

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:30:00 ; Search time 39 Seconds
(without alignments)
695.758 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDERQMAISGGFIRRVINA.....SNKTRIDEANQATKMLGSG 86

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_muc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	57.0	124	13	093578 brachydanio
2	49	57.0	143	6	Q9GM34 macaca fasc
3	32	37.2	206	13	Q8AXM2 Q8axm2 xenopus lae
4	32	37.2	206	13	Q8AXM1 Q8axm1 xenopus lae
5	22	25.6	203	13	093579 brachydanio
6	10	11.6	210	11	Q35620 mus musculus
7	10	11.6	210	11	Q70377 rattus norv
8	10	11.6	210	11	Q09044 mus musculus
9	10	11.6	221	11	Q9D3L3 Q9d3l3 mus musculus
10	9	10.5	204	13	Q8JIS7 Q8jis7 xenopus lae
11	9	10.5	214	13	Q7ZVE4 Q7zev4 brachydanio
12	8	9.3	90	5	096578 leucophaea
13	8	9.3	125	5	096576 leucophaea
14	8	9.3	156	16	Q892G6 Q892g6 clostridium
15	8	9.3	158	5	096575 leucophaea
16	8	9.3	195	5	096574 leucophaea

17	8	9.3	357	16	Q99W76
18	8	9.3	593	16	Q24909
19	8	9.3	1135	5	Q9NJ04
20	7	8.1	74	10	Q93VM1
21	7	8.1	83	2	Q85432
22	7	8.1	83	2	Q85440
23	7	8.1	83	2	Q85439
24	7	8.1	83	2	Q85431
25	7	8.1	162	16	Q8DF43
26	7	8.1	170	10	Q9SBC2
27	7	8.1	171	10	Q9ZSW8
28	7	8.1	197	2	P95796
29	7	8.1	212	5	Q44419
30	7	8.1	212	5	Q76338
31	7	8.1	226	11	Q9CVN5
32	7	8.1	228	4	Q8NA63
33	7	8.1	271	4	Q8NQ1
34	7	8.1	285	16	Q926K3
35	7	8.1	303	11	Q9D9D5
36	7	8.1	350	16	Q97EN6
37	7	8.1	380	16	Q8X9Q9
38	7	8.1	384	16	Q836N1
39	7	8.1	387	16	Q9CJ77
40	7	8.1	393	2	Q8GR72
41	7	8.1	396	16	Q8U6M7
42	7	8.1	407	16	Q7TV99
43	7	8.1	414	5	Q93231
44	7	8.1	473	10	Q8S029
45	7	8.1	562	13	Q7SZP4

ALIGNMENTS

RESULT 1
093578 PRELIMINARY; PRT; 124 AA.
AC 093578
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN SNAP25A OR SNAP
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99057281; PubMed=9843147;
RA Rislinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage.";
RL J. Neurosci. Res. 54:563-573(1998).
DR EMBL; AF091593; AAC64289.1; -;
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t_SNARE; 1.
DR PROSITE; PS50192; T_SNARE; 1.
FT NON TER
FT 1
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 57.0%; Score 49; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 5.3e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDKCNRIDTQNRQIDRIMEKADSNKTRIDEANQATKMLGSG 86

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Db      76 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 124
|||||
RESULT 2
Q9GM34  Q9GM34      PRELIMINARY;      PRT;      143 AA.
AC      Q9GM34;
DT      01-MAR-2001 (TReMBLrel. 16, Created)
DT      01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC      Cercopithecinae; Macaca.
OX      NCBI_TaxID=9541;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA      Suzuki Y., Sugano S., Hashimoto K.;
RT      "Isolation of full-length cDNA clones from macaque brain cDNA
RT      libraries";
RL      Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB049852; BAB16738.1; -.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T SNARE.
DR      Pfam; PF00835; SNAP-25; 1.
DR      Pfam; PF05739; SNARE; 1.
DR      SMART; SM00397; t SNARE; 1.
DR      PROSITE; PS50192; t SNARE; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 143 AA; 16043 MW; D625DBAAA0893FB0 CRC64;

Query Match      57.0%; Score 49; DB 6; Length 143;
Best Local Similarity 100.0%; Pred. No. 6e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 86
|||||
Db      95 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 143
|||||

RESULT 3
Q9AXM2  Q9AXM2      PRELIMINARY;      PRT;      206 AA.
AC      Q9AXM2;
DT      01-MAR-2003 (TReMBLrel. 23, Created)
DT      01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      SNAP25a.
OS      Xenopus laevis (African clawed frog).
OC      Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RA      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF335586; AA013788.1; -.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T SNARE.
DR      Pfam; PF00835; SNAP-25; 1.
DR      Pfam; PF05739; SNARE; 1.
DR      SMART; SM00397; t SNARE; 2.
DR      PROSITE; PS50192; t SNARE; 2.
SQ      SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match      37.2%; Score 32; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. No. 9.8e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNK 69
|||||
Db      158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNK 189
|||||

RESULT 4
Q9AXM1  Q9AXM1      PRELIMINARY;      PRT;      206 AA.
AC      Q9AXM1;
DT      01-MAR-2003 (TReMBLrel. 23, Created)
DT      01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE      SNAP25b (Hypothetical protein).
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RA      Klein S., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RA      Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB049852; BAB16738.1; -.
DR      InterPro; IPR000928; SNAP-25.
DR      InterPro; IPR000727; T SNARE.
DR      Pfam; PF00835; SNAP-25; 1.
DR      Pfam; PF05739; SNARE; 1.
DR      SMART; SM00397; t SNARE; 2.
DR      PROSITE; PS50192; t SNARE; 2.
SQ      SEQUENCE 206 AA; 23187 MW; 7D3B20717B577F02 CRC64;

Query Match      37.2%; Score 32; DB 13; Length 206;
Hypothetical protein.
SQ      SEQUENCE 206 AA; 23187 MW; 7D3B20717B577F02 CRC64;

Query Match      37.2%; Score 32; DB 13; Length 206;
Hypothetical protein.
SQ      SEQUENCE 206 AA; 23187 MW; 7D3B20717B577F02 CRC64;

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Best Local Similarity 100.0%; Pred. No. 9.8e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWDGNEIDTQNRQIDRIMEKADSNK 69
DB 158 GNLHWDGNEIDTQNRQIDRIMEKADSNK 189

RESULT 5
O93579 ID O93579 PRELIMINARY; PRT; 203 AA.
AC O93579;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein 25.2)
GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammer D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage";
RL J. Neurosci. Res. 0:0-0(1998).
DR EMBL; AF091594; AAC64290.1; -;
DR EMBL; AF091596; AAC73007.1; -;
DR ZFIN; ZDB-GENE-980526-392; snap25b.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS0192; t SNARE; 2.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DDC93F38 CRC64;

Query Match 25.6%; Score 22; DB 13; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ADSNKTIDEANQRATKMLGSG 86
DB 182 ADSNKTIDEANQRATKMLGSG 203

RESULT 6
O35620 ID O35620 PRELIMINARY; PRT; 210 AA.
AC O35620;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 23kDa synaptosomal associated protein.
GN SNAP23 OR MSNAP-23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen S.K., Doerre S., Corley R.B.;
RT "SNARE expression in mouse plasma cells";
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007169; AAB62932.1; -;
DR MGD; MGI:109356; Snap23.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.

DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS0192; t SNARE; 2.
SQ SEQUENCE 210 AA; 23277 MW; FB752FB58D5AE6D9 CRC64;

Query Match 11.6%; Score 10; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
DB 168 MALDMGNEID 177

RESULT 7
O70377 ID O70377 PRELIMINARY; PRT; 210 AA.
AC O70377;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SNAP-23.
GN SNAP-23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95162237; PubMed=10051443;
RA St-Denis J.F., Cabanols J.P., Cushman S.W., Roche P.A.;
RT "SNAP-23 participates in SNARE complex assembly in rat adipose
RT cells";
RL Biochem. J. 338:709-715(1999).
DR EMBL; AF052596; AAC06031.1; -;
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t SNARE; 2.
DR PROSITE; PS0192; t SNARE; 2.
SQ SEQUENCE 210 AA; 23235 MW; OD63E3A6F9FE3BA2 CRC64;

Query Match 11.6%; Score 10; DB 11; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
DB 168 MALDMGNEID 177

RESULT 8
O09044 ID O09044 PRELIMINARY; PRT; 210 AA.
AC O09044;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SYNDET (SNAP-23) (Synaptosomal-associated protein, 23KD).
GN SNAP23 OR SNT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat;
RX MEDLINE=97312558; PubMed=9168999;
RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,
RA Niki T., Okazawa H., Kubota T., Kasuga M.;
RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c";

RL Biochem. Biophys. Res. Commun. 234:257-262 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97220227; PubMed=9067602;
 RA Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,
 RA Baldini G.;
 RT "Syndet is a novel SNAP-25 related protein expressed in many
 RT tissues";
 RL J. Cell Sci. 110:505-513 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Brownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 DR EMBL; AB000822; BAA20345.1; -;
 DR EMBL; U73143; AB53597.1; -;
 DR EMBL; AF213257; AAF23503.1; -;
 DR EMBL; AF213251; AAF23503.1; JOINED.
 DR EMBL; AF213252; AAF23503.1; JOINED.
 DR EMBL; AF213253; AAF23503.1; JOINED.
 DR EMBL; AF213254; AAF23503.1; JOINED.
 DR EMBL; AF213255; AAF23503.1; JOINED.
 DR EMBL; AF213256; AAF23503.1; JOINED.
 DR EMBL; AK019162; BAB31577.1; -;
 DR PIR; JC5512; JC5512.
 DR MGD; MGI:109356; Snap23.
 DR InterPro; IPR000928; SNAP-25.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS50192; t_SNARE; 2.
 SQ SEQUENCE 210 AA; 23261 MW; 6919127E16BA2C9 CRC64;
 Query Match 11.6%; Score 10; DB 11; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 MALDGMNEID 52
 |||||
 DB 168 MALDGMNEID 177
 RESULT 9
 Q9D3L3 PRELIMINARY; PRT; 221 AA.
 AC Q9D3L3;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Synaptonemal-associated protein, 23kD.
 GN SNAP23.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 DR EMBL; AK017311; BAB30686.1; -;
 DR MGD; MGI:109356; Snap23.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; t_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS50192; t_SNARE; 2.
 SQ SEQUENCE 221 AA; 24550 MW; 368862BE7232DEFB CRC64;
 Query Match 11.6%; Score 10; DB 11; Length 221;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 MALDGMNEID 52
 |||||
 DB 179 MALDGMNEID 188
 RESULT 10
 Q8JIS7 PRELIMINARY; PRT; 204 AA.
 AC Q8JIS7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP-23.
 GN XOSNAP-23.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mashima J., Nagahama M., Hasegawa K., Tani K., Kikuchi F.,
 RA Horigome T., Yamamoto A., Tagaya M.;
 RT "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion
 RT of nuclear membrane vesicles";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033718; BAC06591.1; -;

DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 1.
 DR PROSITE; PS50192; T_SNARE; 2.
 SQ SEQUENCE 204 AA; 22771 MW; D034F75E638E8805 CRC64;
 Query Match 10.5%; Score 9; DB 13; Length 204;
 Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 68 NKTRIDEAN 76
 Db 188 NKTRIDEAN 196
 RESULT 11
 Q7ZVE4
 ID Q7ZVE4 PRELIMINARY; PRT; 214 AA.
 AC Q7ZVE4;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DE Similar to synaptosomal-associated protein, 23 kDa.
 DE Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OS NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Body;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC045896; AAH45896.1; -.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS50192; T_SNARE; 2.
 SQ SEQUENCE 214 AA; 23670 MW; 5B43808BA6645A4C CRC64;
 Query Match 10.5%; Score 9; DB 13; Length 214;
 Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 44 ALDMGNEID 52
 Db 175 ALDMGNEID 183
 RESULT 12
 Q96578
 ID Q96578 PRELIMINARY; PRT; 90 AA.
 AC Q96578;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DE Synaptosome-associated protein SNAP-25-5 (fragment).
 DE SNAP-5.
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OS NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99259578; PubMed=10327594;
 RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
 RT "The highly conserved synapse protein SNAP-25 displays sequence variability in the cockroach Leucophaea maderae.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR SMART; SM00397; t_SNARE; 1.
 DR PROSITE; PS50192; T_SNARE; 1.
 SQ SEQUENCE 90 AA; 10136 MW; E502D8954676E9F7 CRC64;
 Query Match 9.3%; Score 8; DB 5; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 QNRQIDRI 61
 Db 60 QNRQIDRI 67
 RESULT 13
 Q96576
 ID Q96576 PRELIMINARY; PRT; 125 AA.
 AC Q96576;
 DT 01-MAY-1999 (TRENBLrel. 10, Created)
 DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
 DE Synaptosome-associated protein SNAP-25-3 (fragment).
 DE SNAP-3.
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OS NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=99259578; PubMed=10327594;
 RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
 RT "The highly conserved synapse protein SNAP-25 displays sequence variability in the cockroach Leucophaea maderae.";
 RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
 DR EMBL; AF091600; AAC69876.1; -.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR SMART; SM00397; t_SNARE; 1.
 DR PROSITE; PS50192; T_SNARE; 1.
 FT NON TER 1
 SQ SEQUENCE 125 AA; 13985 MW; 72B032879858C316 CRC64;
 Query Match 9.3%; Score 8; DB 5; Length 125;
 Best Local Similarity 100.0%; Pred. No. 2.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 QNRQIDRI 61
 Db 94 QNRQIDRI 101
 RESULT 14
 Q892G6
 ID Q892G6 PRELIMINARY; PRT; 156 AA.
 AC Q892G6;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DE Phase-related protein.
 DE CTC02133.
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OS NCBI_TaxID=1513;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
RL EMBL; AF015943; AAC66629.1; -.
RW Complete proteome.
SQ SEQUENCE 156 AA; 17919 MW; FC226BEAD767CE55 CRC64;

Query Match          9.3%; Score 8; DB 16; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 33 VSGILGNL 40
DB 63 VSGILGNL 70

RESULT 15
O96575 PRELIMINARY; PRT; 158 AA.
AC O96575;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-2 (Fragment).
GN SNAP-2.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
RL EMBL; AF01599; AAC69875.1; -.
RW Hypothetical protein MW0482.
SQ SEQUENCE 158 AA; 17926 MW; 6AEE26EBA70D0358 CRC64;

Query Match          9.3%; Score 8; DB 5; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QNRQIDRI 61
DB 109 QNRQIDRI 116

RESULT 16
O96574 PRELIMINARY; PRT; 195 AA.
AC O96574;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein SNAP-25-1.
GN SNAP-1.
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99259578; PubMed=10327594;
RA Johard H.A., Risinger C., Nassel D.R., Larhammar D.;
RT "The highly conserved synapse protein SNAP-25 displays sequence
RT variability in the cockroach Leucophaea maderae.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999).
RL EMBL; AF01598; AAC69874.1; -.
RW Hypothetical protein MW0482.
SQ SEQUENCE 195 AA; 21759 MW; 7DB7C1790EC84151 CRC64;

Query Match          9.3%; Score 8; DB 5; Length 195;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QNRQIDRI 61
DB 182 QNRQIDRI 189

RESULT 17
O99W76 PRELIMINARY; PRT; 357 AA.
AC O99W76;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MW0527 (Hypothetical protein MW0482).
GN SAV0527 OR SA0485 OR MW0482.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 196620;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50, and N315;
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
RW EMBL; AP003359; BAB56689.1; -.
DR EMBL; AP003130; BAB41715.1; -.
DR EMBL; AP004823; BAB94347.1; -.
DR FIR; H9819; H9819.
DR InterPro; IPR002716; PIN.
DR InterPro; IPR006596; PINC.
DR InterPro; IPR002792; TRAM.

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DR Pfam; PF01850; PIN; 1.
DR Pfam; PF01938; TRAM; 1.
DR SMART; SM00670; PIN; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 357 AA; 39586 MW; 7F81D25CF53CC6C9 CRC64;

Query Match 9.3%; Score 8; DB 16; Length 357;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FIRRVTNA 20
Db 60 FIRRVTNA 67
|||||

RESULT 18
O24909 ID O24909 PRELIMINARY; PRT; 593 AA.
AC O24909;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein HP0080.
GN HP0080.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97394467; PubMed=9252185;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-P., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.P., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547 (1997).
DR EMBL; AB000529; AAD07151.1; -.
DR PIR; H64529; H64529.
DR TIGR; HP0080; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 593 AA; 65970 MW; 731C02B2EB7C815A CRC64;

Query Match 9.3%; Score 8; DB 16; Length 593;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNLR 41
Db 81 SGILGNLR 88
|||||

RESULT 19
Q9NJQ4 ID Q9NJQ4 PRELIMINARY; PRT; 1135 AA.
AC Q9NJQ4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SEC7-related protein.
GN SEC7.
OS Parametium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC Parametium.
OX NCBI_TaxID=5888;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=298;
RA Nair S., Guerra C.F., Satir P.;
RT "A SEC7-related protein in Parametium."
RL FASEB J. 0:0-0(1999).
DR EMBL; AF129515; AAF36486.1; -.
DR HSSP; Q99418; IPBV.
DR InterPro; IPR00904; Sec7.
DR Pfam; PF01369; Sec7; 1.
DR SMART; SM00222; Sec7; 1.
DR PROSITE; PS50190; SEC7; 1.
SQ SEQUENCE 1135 AA; 132880 MW; A95B0EC5C90A9BDB CRC64;

Query Match 9.3%; Score 8; DB 5; Length 1135;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIMEK 64
Db 675 QIDRIMEK 682
|||||

RESULT 20
Q93VWL ID Q93VWL PRELIMINARY; PRT; 74 AA.
AC Q93VWL;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE P0560B06.24 protein (P0043B10.16 protein).
GN P0560B06.24 OR P0043B10.16.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0560B06."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0043B10."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003281; BAB64757.1; -.
DR EMBL; AP003236; BAB64727.1; -.
DR Gramene; Q93VWL; -.
SQ SEQUENCE 74 AA; 8288 MW; 8218A251C59901E5 CRC64;

Query Match 8.1%; Score 7; DB 10; Length 74;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 MGNEIDT 53
Db 1 MGNEIDT 7
|||||

RESULT 21
O85432 ID O85432 PRELIMINARY; PRT; 83 AA.
AC O85432;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Major outer membrane lipoprotein I (Fragment).
GN OPRI.

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OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 5939;
 RX MEDLINE=89313294; PubMed=2473376;
 RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
 Hannaert V., Hubert J.C.;
 RT "Cloning and analysis of the gene for the major outer membrane
 lipoprotein from Pseudomonas aeruginosa.";
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 5939;
 RX MEDLINE=99069329;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 Cornelis P.;
 RT "Sequence diversity of the oprI gene, coding for major outer membrane
 lipoprotein I, among rRNA group I pseudomonads.";
 RL J. Bacteriol. 180:6551-6556(1998).
 DR EMBL; AF065971; AAD03526.1; -;
 DR InterPro; IPR000437; Prok_lipoprot S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Lipoprotein.
 FT NON TER 83
 SQ SEQUENCE 83 AA; 8683 MW; DDE5436ED924DBA9 CRC64;
 Query Match 8.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 73 DEANORA 79
 Db 67 DEANORA 73

RESULT 22
 OS Pseudomonas tolaasii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=29442;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2342;
 RX MEDLINE=89313294; PubMed=2473376;
 RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
 Hannaert V., Hubert J.C.;
 RT "Cloning and analysis of the gene for the major outer membrane
 lipoprotein from Pseudomonas aeruginosa.";
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 2342;
 RX MEDLINE=99069329;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 Cornelis P.;
 RT "Sequence diversity of the oprI gene, coding for major outer membrane
 lipoprotein I, among rRNA group I pseudomonads.";
 RL J. Bacteriol. 180:6551-6556(1998).
 DR EMBL; AF065979; AAD03534.1; -;
 DR InterPro; IPR000437; Prok_lipoprot S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Lipoprotein.

FT NON TER 83
 SQ SEQUENCE 83 AA; 8826 MW; FBSF436ED924DBBA CRC64;
 Query Match 8.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 73 DEANORA 79
 Db 67 DEANORA 73

RESULT 23
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 5833;
 RX MEDLINE=89313294; PubMed=2473376;
 RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
 Hannaert V., Hubert J.C.;
 RT "Cloning and analysis of the gene for the major outer membrane
 lipoprotein from Pseudomonas aeruginosa.";
 RL Mol. Microbiol. 3:421-428(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LMG 5833;
 RX MEDLINE=99069329;
 RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
 Cornelis P.;
 RT "Sequence diversity of the oprI gene, coding for major outer membrane
 lipoprotein I, among rRNA group I pseudomonads.";
 RL J. Bacteriol. 180:6551-6556(1998).
 DR EMBL; AF065978; AAD03533.1; -;
 DR InterPro; IPR000437; Prok_lipoprot S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Lipoprotein.
 FT NON TER 83
 SQ SEQUENCE 83 AA; 8826 MW; FBSF436ED924DBBA CRC64;
 Query Match 8.1%; Score 7; DB 2; Length 83;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 73 DEANORA 79
 Db 67 DEANORA 73

RESULT 24
 OS Pseudomonas corrugata.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=47879;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=LWG 2172;
RX MEDLINE=89313294; PubMed=2473376;
RA Cornelis P., Bouia A., Belarbi A., Guyonvarch A., Kammerer B.,
RT Hannaert V., Hubert J.C.;
RA "Cloning and analysis of the gene for the major outer membrane
RT lipoprotein from Pseudomonas aeruginosa.";
RL Mol. Microbiol. 3:421-428(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LWG 2172;
RX MEDLINE=99069329;
RA De Vos D., Bouton C., Sarniguet A., De Vos P., Vauterin M.,
RT Cornelis P.;
RT "Sequence diversity of the oprI gene, coding for major outer membrane
RT lipoprotein I, among rRNA group I pseudomonads.";
RL J. Bacteriol. 180:6551-6556(1998).
DR EMBL; AF065970; AA003525.1; -
DR InterPro; IPR000437; Prok_lipoprot_S.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Lipoprotein.
FT NON TER 83
SQ SEQUENCE 83 AA; 8796 MW; 929438A81549DBAC CRC64;

Query Match 8.1%; Score 7; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 DEANORA 79
DB 67 DEANORA 73

RESULT 25
Q8DF43
ID Q8DF43 PRELIMINARY; PRT; 162 AA.
AC Q8DF43;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN VV10381.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF016798; AA008905.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 162 AA; 18029 MW; 65272C082012A474 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 162;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ANQRATK 81
DB 124 ANQRATK 130

RESULT 26
Q9SBC2
ID Q9SBC2 PRELIMINARY; PRT; 170 AA.
AC Q9SBC2;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
OS Hamamelis virginiana.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Hamamelidaceae; Hamamelis.
OX NCBI_TaxID=4397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Szpara M.L.T.;
RT "Isolation of invertase gene sequences from witch hazel (Hamamelis
RT virginiana)";
RL Thesis (1998); Pennsylvania State University.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AF091546; AAC99429.1; -
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001362; Glyco_hydro_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR SMART; SM00640; Glyco_32; 1.
KW Glycoprotein; Glycosidase; Hydrolase.
FT NON TER 1
FT NON TER 170
SQ SEQUENCE 170 AA; 19356 MW; BE388990C7236D31 CRC64;

Query Match 8.1%; Score 7; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 IDTQNRQ 57
DB 67 IDTQNRQ 73

RESULT 27
Q9ZSW8
ID Q9ZSW8 PRELIMINARY; PRT; 171 AA.
AC Q9ZSW8;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Beta-fructofuranosidase (EC 3.2.1.26) (Fragment).
OS Hamamelis virginiana.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Hamamelidaceae; Hamamelis.
OX NCBI_TaxID=4397;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Szpara M.L.T.;
RT "Isolation of invertase gene sequences from witch hazel (Hamamelis
RT virginiana)";
RL Thesis (1998); Pennsylvania State University.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AF091545; AAC99428.1; -
DR GO; GO:0004564; F:beta-fructofuranosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001362; Glyco_hydro_32.
DR Pfam; PF00251; Glyco_hydro_32; 1.
DR SMART; SM00640; Glyco_32; 1.
KW Glycoprotein; Glycosidase; Hydrolase.
FT NON TER 1
FT NON TER 171
SQ SEQUENCE 171 AA; 19494 MW; B5D4EFB5C0798FEC CRC64;

Query Match 8.1%; Score 7; DB 10; Length 171;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 IDTQNRQ 57
DB 68 IDTQNRQ 74

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RESULT 28

P95796
 ID P95796 PRELIMINARY; PRT; 197 AA.
 AC P95796
 DT 01-MAY-1997 (TRENBLrel. 03, Created)
 DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Seriatia marcescens.
 OG Plasmid R478.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Seriatia.
 OX NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Whelan K.F., Bekkering M., Taylor D.E.;
 RT "Analysis of the region upstream of terZ in plasmid R478.";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U59239; AAB37123.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 197 AA; 22154 MW; C98FA5589FC97840 CRC64;

Query Match 8.1%; Score 7; DB 2; Length 197;

Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RVTNAR 21

Db 150 RVTNAR 156
 |||||

RESULT 29

O44419
 ID O44419 PRELIMINARY; PRT; 212 AA.
 AC O44419
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Synaptosomal-associated protein 25.
 OS SNAP-25.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98406073; PubMed=9733723;
 RA Schulz J.R., Sasaki J.D., Vacquier V.D.;
 RT "Increased association of synaptosome-associated protein of 25 kDa
 with syntaxin and vesicle-associated membrane protein following
 RT acrosomal exocytosis of sea urchin sperm.";
 RL J. Biol. Chem. 273:24355-24359(1998).
 DR EMBL; AF036902; AAC35867.1; -.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 2.
 DR SMART; SM00397; t SNARE; 2.
 DR PROSITE; PS50192; T SNARE; 2.
 SQ SEQUENCE 212 AA; 24108 MW; 47C1EB69459F250A CRC64;

Query Match 8.1%; Score 7; DB 5; Length 212;

Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMA 44

Db 164 GNLRHMA 170
 |||||

RESULT 30

O76338
 ID O76338 PRELIMINARY; PRT; 212 AA.
 AC O76338
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Ovarian synaptosome-associated protein 25 homolog.
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=99057936; PubMed=9837952;
 RA Tahara M., Coorsen J.R., Timmers K., Blank P.S., Whalley T.,
 RA Scheller R., Zimmerberg J.;
 RT "Calcium can disrupt the SNARE protein complex on sea urchin egg
 RT secretory vesicles without irreversibly blocking fusion.";
 RL J. Biol. Chem. 273:33667-33673(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Kolosova I.A., Timmers K., Kingsley D.H., Bezrukov L., Zimmerberg J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF061750; AAC83577.1; -.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 2.
 DR SMART; SM00397; t SNARE; 2.
 DR PROSITE; PS50192; T SNARE; 2.
 SQ SEQUENCE 212 AA; 24014 MW; E1B9EDB43C056AD7 CRC64;

Query Match 8.1%; Score 7; DB 5; Length 212;

Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMA 44

Db 164 GNLRHMA 170
 |||||

RESULT 31

Q9CVN5
 ID Q9CVN5 PRELIMINARY; PRT; 226 AA.
 AC Q9CVN5
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE 1700035F04RIK protein (Fragment).
 GN 1700035F04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
DR EMBL; AK007251; BAB24916.1; --
DR MGD; MGI:1914606; 1700095F04Rik.
FT NON TER 226 226
SQ SEQUENCE 226 AA; 26797 MW; 90EA1783E4675997 CRC64;

Query Match 8.1%; Score 7; DB 11; Length 226;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
DB 41 RIDEANQ 47

RESULT 32
Q8NA63 PRELIMINARY; PRT; 228 AA.
AC Q8NA63;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein FLJ35807.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Testis;
RC Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato K., Wakanatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Magatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahori K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK093126; BAC04065.1; --
KW Hypothetical protein.
SQ SEQUENCE 228 AA; 26968 MW; 7F0AFA085E65887D CRC64;

Query Match 8.1%; Score 7; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
DB 26 RIDEANQ 32

RESULT 33
Q8N601 PRELIMINARY; PRT; 271 AA.
AC Q8N601;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Similar to RIKEN cDNA 1700095F04 gene.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Straubeig R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029221; AAH29221.1; --
SQ SEQUENCE 271 AA; 32319 MW; 3AB387A2DC98712 CRC64;

Query Match 8.1%; Score 7; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQ 77
DB 9 RIDEANQ 15

RESULT 34
Q926K3 PRELIMINARY; PRT; 285 AA.
AC Q926K3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein pII0057.
GN pII0057.
OS Listeria innocua.
OG Plasmid pII100.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshhi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR EMBL; AL592102; CAC42055.1; --
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 285 AA; 32850 MW; 92982A93BD476332 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 285;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIME 63
DB 254 QIDRIME 260

RESULT 35
Q9D9D5 PRELIMINARY; PRT; 303 AA.
AC Q9D9D5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1700095F04Rik protein (RIKEN cDNA 1700095F04).
GN 1700095F04Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gotojori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staublei F., Suzuki R., Tomita M., Wagner D., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayaishizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan A., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testicle;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK07078; BAB24853.1; -;
 DR EMBL; BC049568; AAH49568.1; -;
 DR MGD; MGI:1914606; 1700095F04Rik.
 SQ SEQUENCE 303 AA; 35853 MW; D4AA3952B5C10586 CRC64;
 Query Match 8.1%; Score 7; DB 11; Length 303;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 71 RIDEANQ 77
 DB 41 RIDEANQ 47
 RESULT 36
 Q97EN6 PRELIMINARY; PRT; 350 AA.
 ID Q97EN6
 AC Q97EN6;

DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mannose-1-phosphate guanylyltransferase.
 GN CAC3072.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286; Makarova K.S., Zeng Q.,
 RA Noelling J., Breston G., Omeichenko M.V., Hitti J., Wolf Y.I.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 193:4823-4838(2001).
 RL EMBL; AE007804; AAK91012.1; -;
 DR PIR; A97278; A97278.
 DR GO; GO:0005509; P:calcium ion binding; IEA.
 DR GO; GO:0016779; P:nucleotidyltransferase activity; IEA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:ribosynthesis; IEA.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR005835; NTP transferase.
 DR Pfam; PF00483; NTP transferase; 1.
 DR PROSITE; PS00018; EF HAND; 1.
 KW Transferase; Nucleotidyltransferase; Complete proteome.
 SQ SEQUENCE 350 AA; 39884 MW; 0925415F6152C252 CRC64;
 Query Match 8.1%; Score 7; DB 16; Length 350;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 IMEKADS 67
 DB 254 IMEKADS 260
 RESULT 37
 Q8X9Q9 PRELIMINARY; PRT; 380 AA.
 ID Q8X9Q9
 AC Q8X9Q9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein zll169.
 GN Zll169 OR Z1608 OR ECS1349.
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=83334;
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Ferna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaoka C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
 O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 DR EMBL; AE005309; AAG55723.1; -;
 DR EMBL; AE005273; AAG55314.1; -;
 DR EMBL; AP002554; BAB34772.1; -;
 DR PIR; E90797; E90797.
 DR PIR; G85657; G85657.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 380 AA; 42005 MW; E58261986A615927 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 380;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 RVTNAR 21
 Db 150 RVTNAR 156
 |||||

RESULT 38
 ID Q836N1 PRELIMINARY; PRT; 384 AA.
 AC Q836N1;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Multidrug resistance protein, putative.
 GN EFl078.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=V583 / ATCC 700802;
 RX MEDLINE=22550857; PubMed=12663927;
 RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
 RA Tettelin H., Dodson R.J., Unayam L., Brinkay L., Beanan M.,
 RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
 RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
 RT "Role of mobile DNA in the evolution of vancomycin-resistant
 RT Enterococcus faecalis";
 RL Science 299:2071-2074(2003).
 DR EMBL; AE016950; AA080880.1; -;
 DR TIGR; EFl078; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0015520; P:tetracycline:hydrogen antiporter activity; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0015904; P:tetracycline transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR InterPro; IPR001958; TCR TetA.
 DR Pfam; PF00083; sugar tr; 1.
 DR PRINTS; PR01035; TCRTEA.
 DR PROSITE; PS00850; MFS; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 384 AA; 41284 MW; 67622D5D5D7196EB8 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 384;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AISGGFI 14
 |||||

Db 138 AISGGFI 144
 |||||

RESULT 39
 ID Q9CU77 PRELIMINARY; PRT; 387 AA.
 AC Q9CU77;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Multidrug efflux transporter.
 GN BLT OR Lf0123.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=1137471;
 RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malarre K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium *Lactococcus*
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006250; AAK04221.1; -;
 DR PIR; C86640; C86640.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0015520; P:tetracycline:hydrogen antiporter activity; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0015904; P:tetracycline transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub transporter.
 DR InterPro; IPR005829; Sug transporter.
 DR InterPro; IPR001958; TCR TetA.
 DR Pfam; PF00083; sugar tr; 1.
 DR PRINTS; PR01035; TCRTEA.
 DR PROSITE; PS00850; MFS; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 387 AA; 41671 MW; A3E991E0C39C71A6 CRC64;

Query Match 8.1%; Score 7; DB 16; Length 387;
 Best Local Similarity 100.0%; Pred. No. 65;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AISGGFI 14
 |||||

Db 138 AISGGFI 144
 |||||

RESULT 40
 ID Q8GR72 PRELIMINARY; PRT; 393 AA.
 AC Q8GR72;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Multidrug efflux pump.
 GN EMEA.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29212;
 RA Lee E., Kuroda T., Morita Y., Mizushima T., Tsuchiya T.;
 RT "Enterococcus faecalis ATCC29212 emeA gene for multidrug resistance
 RT pump, complete cds.";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB091338; BAC11911.1; -;

DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0015520; P: tetracycline hydrogen antiporter activity; IEA.
 DR GO: GO:0005213; P: tetracycline transport; IEA.
 DR GO: GO:0015904; P: tetracycline transport; IEA.
 DR GO: GO:0006810; P: transport; IEA.
 DR InterPro: IPR007114; NPS.
 DR InterPro: IPR005828; Sub transporter.
 DR InterPro: IPR005829; Sug transporter.
 DR InterPro: IPR001958; TCR_TetA.
 DR Pfam: PF00083; sugar tr; 1.
 DR PRINTS: PR01035; TCR_TetA.
 DR PROSITE: PS00850; NPS; 1.
 DR PROSITE: PS00216; SUGAR TRANSPORT 1; 1.
 SQ SEQUENCE 393 AA; 42082 MW; 7614EAFB8A748088 CRC64;

Query Match 8.1%; Score 7; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AISGGFI 14
 DB 138 AISGGFI 144
 |||||

RESULT 41
 ID Q8UGM7 PRELIMINARY; PRT; 396 AA.
 AC Q8UGM7;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein Atu4780.
 GN ATU4780 OR AGR L.206.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goettner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Homiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328 (2001).
 DR EMBL: AE009406; AL45574.1; ALT_INIT.
 DR EMBL: AE008208; AAK98669.1; -.
 DR PIR: AH3144; AH3144.
 DR PIR: C98143; C98143.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 396 AA; 40524 MW; 45951B6300A1017A CRC64;

Query Match 8.1%; Score 7; DB 16; Length 396;

Best Local Similarity 100.0%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNL 40
 DB 261 SGILGNL 267
 |||||

RESULT 42
 ID Q7TV99 PRELIMINARY; PRT; 407 AA.
 AC Q7TV99;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE tRNA-(guanine-N1)-methyltransferase fused to 2-C-methyl-D-erythritol
 DE 2,4-cyclodiphosphate synthase.
 GN TRMD/ISPF OR PRO1354.
 OS Prochlorococcus marinus.
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=1219;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=SARG / CCMP 1375 / SS120;
 RX MEDLINE=22810154; PubMed=12917486;
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,
 RA Makarova K.S., Ostrowski M., Ozcas S., Robert C., Rogozin I.B.,
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
 RA Wolf Y.I., Hess W.R.;
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,
 a nearly minimal oxyphototrophic genome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).
 DR EMBL: AB017165; AAQ00398.1; -.
 KW Methyltransferase; transferase; Complete proteome.
 SQ SEQUENCE 407 AA; 45243 MW; 59278101AD67707C CRC64;

Query Match 8.1%; Score 7; DB 16; Length 407;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRID 73
 DB 234 SNKTRID 240
 |||||

RESULT 43
 ID Q93231 PRELIMINARY; PRT; 414 AA.
 AC Q93231;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein Cl7E4.10.
 GN Cl7E4.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Percy C.M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018 (1998).
 DR EMBL: Z81037; CAB02748.2; -.
 DR PIR: T19354; T19354.

```

DR WormPep; C17E4.10; CE32589.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD REPEATS_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 414 AA; 47535 MW; 2095705E25CF4C59 CRC64;

  Query Match      8.1%; Score 7; DB 5; Length 414;
  Best Local Similarity 100.0%; Pred. No. 69;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 ENEMEDE 28
      |||||
Db      248 ENEMEDE 254

RESULT 44
Q8S0Z9 PRELIMINARY; PRT; 473 AA.
AC Q8S0Z9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P0445E10.22 protein (P0478H03.16 protein).
GN P0445E10.22 OR P0478H03.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriatoidae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
  clone:P0445E10.22";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
  clone:P0478H03.16";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003347; BAB86062.1; -.
DR EMBL; AP003452; BAB92700.1; -.
DR Gramene; Q8S0Z9;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; F:transporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0006855; P:multidrug transport; IEA.
DR InterPro; IPR002528; Mate.
DR Pfam; PF01554; Mate; 2.
DR TIGRFAMs; TIGR00797; mate; 1.
SQ SEQUENCE 473 AA; 51131 MW; 44427CCFA66353FE CRC64;

  Query Match      8.1%; Score 7; DB 10; Length 473;
  Best Local Similarity 100.0%; Pred. No. 77;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      67 SNKTRID 73
      |||||
Db      437 SNKTRID 443

RESULT 45
Q7SZP4 PRELIMINARY; PRT; 562 AA.
AC Q7SZP4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056314; AAH56314.1; -.
KW Hypothetical protein.
SQ SEQUENCE 562 AA; 64750 MW; 811AA64F5B30F9FB CRC64;

  Query Match      8.1%; Score 7; DB 13; Length 562;
  Best Local Similarity 100.0%; Pred. No. 90;
  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      63 EKADSNK 69
      |||||
Db      546 EKADSNK 552

Search completed: March 4, 2004, 08:34:12
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:29:20 ; Search time 14 Seconds
(without alignments)
319.860 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGFIIRVTNA.....SNKTRIDEANQATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	49	57.0	204	1 SN2A CARAU	P36977 Carassius a
2	49	57.0	206	1 SN25 HUMAN	P13795 homo sapien
3	25	29.1	203	1 SN2B CARAU	P13798 Carassius a
4	15	17.4	54	1 SN25 RABIT	P55820 ocyctolagus
5	10	11.6	210	1 SN25 TORMA	P36976 torpedo mar
6	8	9.3	212	1 SN25 DROME	P36975 drosophila
7	7	8.1	422	1 ERIA METJA	Q8p98 methanosarc
8	6	7.0	138	1 C141 HUMAN	Q9y3e0 homo sapien
9	6	7.0	138	1 C141 MOUSE	Q9cr60 mus musculu
10	6	7.0	141	1 MLR4 SCHPO	Q09196 schizosacch
11	6	7.0	147	1 RM28 YEAST	P36527 saccharomyc
12	6	7.0	149	1 ARGR LISIN	Q92by8 listeria in
13	6	7.0	149	1 ARGR LISMO	Q8y7b9 listeria mo
14	6	7.0	152	1 YBB6 PSEAE	Q9hv53 pseudomonas
15	6	7.0	157	1 YGAO BACSU	P97029 bacillus su
16	6	7.0	168	1 YB56 HAEIN	P44203 haemophilus
17	6	7.0	175	1 ATPF CHLRE	Q8ht15 chlamydomon
18	6	7.0	178	1 RAC2 PRGST	O52424 providencia
19	6	7.0	199	1 TRPF CAMJE	Q9pf53 campylobact
20	6	7.0	200	1 YB15 HUMAN	P44187 haemophilus
21	6	7.0	201	1 CERL HUMAN	Q9ntu7 homo sapien
22	6	7.0	201	1 COAE CLOAB	Q97k22 clostridium
23	6	7.0	225	1 WRED METKA	O32864 methanopyru
24	6	7.0	236	1 YW2 YEAST	P40586 saccharomyc
25	6	7.0	238	1 KF5C RAT	P56536 rattus norv
26	6	7.0	242	1 Y22T AGRVI	O34299 agrobacteri
27	6	7.0	245	1 KDSB FUSNN	O8rfab fusobacteri
28	6	7.0	254	1 RPIA TREPA	O83625 treponema p
29	6	7.0	261	1 YRKJ BACSU	P54437 bacillus su
30	6	7.0	269	1 SET_DROME	P53997 drosophila
31	6	7.0	271	1 ATBP STRAU	P18179 scaphylococ
32	6	7.0	280	1 CTX3 HUMAN	Q9ujql homo sapien
33	6	7.0	281	1 PSTA METJA	Q58419 methanococc

ALIGNMENTS

RESULT 1

ID	SN2A CARAU	STANDARD;	PRT;	204 AA.
AC	P36977;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Synaptosomal-associated protein 25A (SNAP-25A).			
GN	SNAP-A.			
OS	Carassius auratus (Goldfish).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Carassius.			
OX	NCBI_TaxID=7957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Retina;			
RX	MEDLINE=94068448; PubMed=8248151;			
RA	Risinger C., Lathammar D.;			
RT	"Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).			
CC	-!- FUNCTION: May play an important role in the synaptic function of specific neuronal systems. Associates with proteins involved in vesicle docking and membrane fusion.			
CC	-!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of the nerve terminal.			
CC	-!- SIMILARITY: Belongs to the SNAP-25 family.			
CC	-!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; L22973; AAA16537.1; -			
DR	PIR; I50480; I50480.			
DR	InterPro; IPR000928; SNAP-25.			
DR	InterPro; IPR000727; t-SNARE.			
DR	Pfam; PF00835; SNAP-25; 1.			
DR	Pfam; PF05739; SNAP; 1.			
DR	SMART; SM00397; t-SNARE; 2.			
DR	PROSITE; P550192; t-SNARE; 2.			
KW	Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.			
FT	DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.			
FT	DOMAIN 138 200 t-SNARE COILED-COIL HOMOMOLOGY 2.			
FT	DOMAIN 85 92 CVS-RICH.			
SQ	SEQUENCE 204 AA; 22843 MW; 458BECFCFC09189 CRC64;			

Query Match 57.0%; Score 49; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

P15009 halobacteri
P20281 haloarcula
Q14232 homo sapien
Q991c8 mus musculu
P47292 mycoplasma
P33164 burkholderi
P74192 synechocyst
Q58465 methanococc
P45065 haemophilus
Q9jta6 neisseria m
Q9jyc4 neisseria m
Q8kb67 chlorobium

34 6 7.0 302 1 R33 HALNI
35 6 7.0 304 1 R33 HALMA
36 6 7.0 305 1 E2BA HUMAN
37 6 7.0 305 1 E2BA MOUSE
38 6 7.0 315 1 GCF MYCGE
39 6 7.0 321 1 PDR BURGE
40 6 7.0 330 1 YC78 SYN3
41 6 7.0 337 1 YA65 METJA
42 6 7.0 351 1 MURG HAEIN
43 6 7.0 352 1 ALR NEIMA
44 6 7.0 352 1 ALR NEIMB
45 6 7.0 383 1 ALR CHLTE

QY 38 GNLRHMDWNEIDTQNRQIDRIMEKADSNKTRIDEANQATFQMLGSG 86
 DB 156 GNLRHMDWNEIDTQNRQIDRIMEKADSNKTRIDEANQATFQMLGSG 204

RESULT 2

SN25 HUMAN STANDARD; PRT; 206 AA.
 AC P33795; P36974; P70557; P70558; Q81XK3; Q96FW2; Q9BR45;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
 GN SNAP25 OR SNAP.

OS Homo sapiens (Human)
 OS Macaca mulatta (Rhesus macaque)
 OS Mus musculus (Mouse)
 OS Rattus norvegicus (Rat), and
 OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606, 9544, 10090, 10116, 9031;
 [1]

RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94156217; PubMed=8112622;
 RA Bark I.C., Wilson M.C.;
 RT "Human cDNA clones encoding two different isoforms of the nerve
 terminal protein SNAP-25";
 RL Gene 139:291-292 (1994).
 [2]

RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=94333829; PubMed=8056350;
 RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
 RT "Cloning and sequence analysis of the human SNAP25 cDNA";
 RL Gene 145:313-314 (1994).
 [3]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Human; TISSUE=Skeletal muscle;
 RX MEDLINE=96332494; PubMed=8760387;
 RA Jagadish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
 RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
 RA Frenkel M.J., Ward C.W.;
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25
 (synaptosomal-associated protein 25) A and B isoforms in addition to
 syntaxin 4 and synaptobrevins 1 and 2";
 RL Biochem. J. 317:945-954 (1996).
 [4]

RP SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clea C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Hammond D.V., Griffiths J.C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharvaish M.H., Leverhulme M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLean K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycaamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,

RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871 (2001).
 [5]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [6]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; TISSUE=Hippocampus;
 RX Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [7]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BA16/C;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 SNAP-25, differentially expressed by neuronal subpopulations";
 RL J. Cell Biol. 109:3039-3052 (1989).
 [8]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 within alcohol-related QTLs";
 RL Mamm. Genome 12:657-663 (2001).
 [9]

RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chorthia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed D.J., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Katanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang J.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hahizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [10]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.L.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC SPECIES=Rat;
RA Kataoka M.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Rat; TISSUE=Brain;
RA Cho A.R., You K.H.;
RL "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
RC SPECIES=Rat; TISSUE=Brain;
RX MEDLINE=99155074; PubMed=10037470;
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
RT "SNARE complex proteins, including the cognate pair VAMP-2 and
RT syntaxin-4, are expressed in cultured oligodendrocytes.";
RN J. Neurochem. 72:988-998 (1999).
RN [14]
RP SEQUENCE FROM N.A.
RC SPECIES=Chicken; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
RA Catelinas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.;
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789 (1991).
RN [15]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC SPECIES=Chicken;
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.;
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76 (1993).
RN [16]
RP PALMITOYLATION.
RC SPECIES=Rat;
RX MEDLINE=93100552; PubMed=1281490;
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
RT methionine-rich polypeptide in rapid axonal transport and a major
Query Match 57.0%; Score 49; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.5e-46;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQDRIMEKADSNKTRIDEANQRATYMLGSG 86
DB 158 GNLRHMDMGNEIDTQNRQDRIMEKADSNKTRIDEANQRATYMLGSG 206
RESULT 3
SN2B_CARAU

ID SN2B_CARAU STANDARD; PRT; 203 AA.
AC P36978;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25B (SNAP-25B).
GN SNAP-B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602 (1993).
CC -1- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -1- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -1- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus,
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -1- SIMILARITY: Belongs to the SNAP-25 family.
CC -1- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22976; AAA16538.1; -.
DR PIR; I50481; I50481.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 2.
DR PROSITE; PS50192; T SNARE; 2.
KW Synaptosome; Neuropeptide; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CYS-RICH.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBEBED37D6D7 CRC64;
Query Match 29.1%; Score 25; DB 1; Length 203;
Best Local Similarity 100.0%; Pred. No. 5.8e-20;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQDRIM 62
DB 155 GNLRHMDMGNEIDTQNRQDRIM 179
RESULT 4
SN25_RABIT
ID SN25_RABIT STANDARD; PRT; 54 AA.
AC P55820;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP
DE (Fragments)).

GN SNAP25 OR SNAP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION
 RC STRAIN=New Zealand white; TISSUE=Eye, and Spinal cord;
 RX MEDLINE=92044785; PubMed=1941090;
 RA Loewy A., Liu W.-S., Baitinger C., Willard M.B.;
 RT "The major 35S-methionine-labeled rapidly transported protein
 RT (superprotein) is identical to SNAP-25, a protein of synaptic
 RT terminals.";
 RL J. Neurosci. 11:3412-3421(1991).
 CC -!- FUNCTION: tSNARE involved in the molecular regulation of
 CC neurotransmitter release. May play an important role in the
 CC synaptic function of specific neuronal systems. Associates with
 CC proteins involved in vesicle docking and membrane fusion (By
 CC similarity).
 CC -!- SUBUNIT: Part of the SNARE core complex containing SNAP25, VAMP2
 CC and SYX1A (By similarity).
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC Neurone; Synaptosome.
 KW NON_CONS 29 30
 FT NON_CONS 45 46
 FT NON_CONS 49 50
 FT NON_CONS 54 AA; 6064 MW; 000147740FEB29C5 CRC64;
 SQ SEQUENCE 54 AA; 6064 MW; 000147740FEB29C5 CRC64;
 Query Match 17.4%; Score 15; DB 1; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDREQMAISGGFIR 15
 DB 31 VDREQMAISGGFIR 45
 RESULT 5
 SN25_TORMA
 ID SN25_TORMA STANDARD; PRT; 210 AA.
 AC P36976;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 OS Torpedo marmorata (Marbled electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hypnosqualea; Pristiogaster; Batoidae;
 OC Torpediniformes; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7788;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Electric lobe;
 RX MEDLINE=94043281; PubMed=8226991;
 RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
 RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
 RL J. Biol. Chem. 268:24408-24414(1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; L22020; AAA49284.1; -.
 DR PIR; I50552; I50552.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T-SNARE.
 DR Pfam; PF00835; SNAP-25_1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS0192; T-SNARE; 2.
 KW Synaptosome; Neurone; Repeat; Coiled coil.
 FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.
 FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.
 FT DOMAIN 88 96 CYS-RICH
 FT SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;
 SQ SEQUENCE 210 AA; 23652 MW; 58FE471A9234B8B1 CRC64;
 Query Match 11.0%; Score 10; DB 1; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHVALDM 47
 DB 165 GNLRHVALDM 174
 RESULT 6
 SN25_DROME
 ID SN25_DROME STANDARD; PRT; 212 AA.
 AC P36975;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaptosomal-associated protein 25 (SNAP-25).
 GN SNAP25.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RX MEDLINE=94043281; PubMed=8226991;
 RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
 RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
 RT "Evolutionary conservation of synaptosome-associated protein 25 kDa
 RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones.";
 RL J. Biol. Chem. 268:24408-24414(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97417485; PubMed=9272858;
 RA Risinger C., Deitcher D.L., Lundell I., Schwarz T.L., Larhammar D.;
 RT "Complex gene organization of synaptic protein SNAP-25 in Drosophila
 RT melanogaster.";
 RL Gene 194:169-177(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=22426071; PubMed=12537574;
 RA Hoskins R.A., Smith C.D., Carlson J.W., Carvalho A.B., Halpern A.,
 RA Kaminker J.S., Kennedy C., Mungall C.J., Sullivan B.A., Sutton G.G.,
 RA Yasuhara J.C., Wakimoto B.T., Myers E.W., Celniker S.E., Rubin G.M.,
 RA Karpen G.H.;
 RT "Heterochromatic sequences in a Drosophila whole-genome shotgun
 RT assembly.";
 RL Genome Biol. 3:RSEARCH0085.1-RESEARCH0085.16(2002).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 CC specific neuronal systems. Associates with proteins involved in
 CC vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 CC the nerve terminal.
 CC -!- TISSUE SPECIFICITY: EXCLUSIVELY FOUND IN BRAIN AND GANGLIA.

```

CC CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC CC -----
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CC CC -----
DR DR EMBL; L22021; AAA16059.1; .
DR DR EMBL; U81153; AAB39757.1; .
DR DR EMBL; U81147; AAB39757.1; JOINED.
DR DR EMBL; U81148; AAB39757.1; JOINED.
DR DR EMBL; U81149; AAB39757.1; JOINED.
DR DR EMBL; U81150; AAB39757.1; JOINED.
DR DR EMBL; U81151; AAB39757.1; JOINED.
DR DR EMBL; U81152; AAB39757.1; JOINED.
DR DR FlyBase; FBgn0011288; Snap25
DR DR GO; GO:0005886; C:plasma membrane; NAS.
DR DR GO; GO:0005486; F: t-SNARE activity; NAS.
DR DR GO; GO:0007269; P: neurotransmitter secretion; NAS.
DR DR GO; GO:0016081; P: synaptic vesicle docking; NAS.
DR DR GO; GO:0016083; P: synaptic vesicle fusion; NAS.
DR DR InterPro; IPR000928; SNAP-25.
DR DR InterPro; IPR000727; t-SNARE.
DR DR Pfam; PF00835; SNAP-25; 1.
DR DR Pfam; PF05739; SNARE; 1.
DR DR SMART; SM00397; t-SNARE; 2.
DR DR PROSITE; PS0192; T-SNARE; 2.
DR DR Synaptosome; Neurone; Repeat; Coiled coil.
DR DR FT DOMAIN 26 88 T-SNARE COILED-COIL HOMOLGY 1.
DR DR FT DOMAIN 148 210 T-SNARE COILED-COIL HOMOLGY 2.
DR DR FT DOMAIN 91 99 CYS-RICH.
DR DR SQ SEQUENCE 212 AA; 23685 MW; BDC90649A1AF3AC8 CRC64;

Query Match 9.3%; Score 8; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 0.29; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 54 QNRQIDRI 61
Db 182 QNRQIDRI 189
|||||

RESULT 7
EF1A METWA STANDARD; PRT; 422 AA.
AC QPUB8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu).
TU OR MW2264.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Goel / Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RC MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baumeister S., Jacob C.,
RA Brueggemann H., Lienert T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RA "The genome of Methanosarcina mazei: evidence for lateral gene
RT transfer between Bacteria and Archaea."
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: This protein promotes the GTP-dependent binding of
CC aminoacyl-tRNA to the A-site of ribosomes during protein

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CC CC biosynthesis.
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC CC EF-Tu/EF-1A subfamily.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL; AE013467; AAM31960.1; .
DR DR HAMAP; MF_00118; -. 1.
DR DR InterPro; IPR004539; EF1_alpha.
DR DR InterPro; IPR000795; EF1_GTPbind.
DR DR InterPro; IPR004160; EFTU_Cterm.
DR DR InterPro; IPR004161; EFTU_D2.
DR DR InterPro; IPR009001; Elong_init_C.
DR DR InterPro; IPR005225; Small_GTP.
DR DR Pfam; PF009000; Translat_factor.
DR DR Pfam; PF00009; GTP_EFTU; 1.
DR DR Pfam; PF03144; GTP_EFTU_D3; 1.
DR DR Pfam; PF03143; GTP_EFTU_D3; 1.
DR DR PRINTS; PR00315; ELONGATNFCT.
DR DR TIGRFAMs; TIGR00483; EF-1_alpha; 1.
DR DR TIGRFAMs; TIGR00231; small_GTP; 1.
DR DR PROSITE; PS00301; EFATOR_GTP; 1.
DR DR Elongation factor; Protein biosynthesis; GTP-binding;
KW Complete proteome.
FT NP_BIND 14 21 GTP (BY SIMILARITY).
FT NP_BIND 91 95 GTP (BY SIMILARITY).
FT NP_BIND 146 149 GTP (BY SIMILARITY).
SQ SEQUENCE 422 AA; 46060 MW; 854FAE284F5A87AA CRC64;

Query Match 8.1%; Score 7; DB 1; Length 422;
Best Local Similarity 100.0%; Pred. No. 6.5; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 31 EQVSGIL 37
Db 163 EQVSGIL 169
|||||

RESULT 8
C141 HUMAN STANDARD; PRT; 138 AA.
ID C141 HUMAN
AC Q9Y3EO; Q9PIR9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0198 protein CGI-141 (HDCW39P).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2072150; PubMed=10810093;
RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT "Identification of novel human genes evolutionarily conserved in
RT Caenorhabditis elegans by comparative proteomics."
RL Genome Res. 10:703-713(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgama;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Anorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
RA Mewes H.-W., Ottenwälder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;

```


"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";
 Genom Res. 11:422-433 (2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dendritic cell;
 RA Zhao Z., Huang X., Li N., Zhu X., Cao X.;
 RT "A novel gene from human dendritic cell."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the UPF0198 family.

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 DR EMBL; AF151899; AAD34136.1; -;
 DR EMBL; AL136571; CAB56506.1; -;
 DR EMBL; AF068292; AAF55181.1; ALT_INIT.
 DR EMBL; BC012455; AAH12455.1; -;
 DR F01; T46908; T46908.
 DR InterPro: IPR007305; Got1.
 DR Pfam; PF04178; Got1; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 33 53 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT CONFLICT 37 37 I -> T (IN REF. 3).
 SQ SEQUENCE 138 AA; 15426 MW; 2EB85823C34EFAFA CRC64;

 Query Match 7.0%; Score 6; DB 1; Length 138;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GFIRRV 17
 Db 107 GFIRRV 112
 |||||
 RESULT 9
 C141 MOUSE STANDARD; PRT; 138 AA.
 AC Q9CR60; 2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical UPF0198 protein CGI-141 homolog.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon, and Tongue;
 RX MEDLINE=22354683; PubMed=1246851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirral L.M., Kanapin A., Matsuoka H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Perce G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,
 RA Sultana R., Takekida Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boriss A., Yangisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: Belongs to the UPF0198 family.

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 CC EMBL; AK018531; BAB31257.2; ALT_INIT.
 DR EMBL; AK009991; BAB26630.1; -;
 DR MGD; MGI:1914214; CGI-141.
 DR InterPro: IPR007305; Got1.
 DR Pfam; PF04178; Got1; 1.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 33 53 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 SQ SEQUENCE 138 AA; 15422 MW; 1BE20294C1C670E5 CRC64;

 Query Match 7.0%; Score 6; DB 1; Length 138;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 12 GFIRRV 17
 Db 107 GFIRRV 112
 |||||
 RESULT 10
 MLR4 SCHPO STANDARD; PRT; 141 AA.
 ID MLR4 SCHPO

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argR family.
CC
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CC
CC EMBL; AL596168; CAC96635.1; -
CC PIR; AC1608; AC1608.
CC ListList; LIN01404; -
CC HAMAP; MF 00173; -; 1.
CC InterPro; IPR001669; Arg_repress.
CC Pfam; PF01316; Arg_repressor; 1.
CC Pfam; PF02863; Arg_repressor; C; 1.
CC PRINTS; PR01467; ARGREPRESSOR.
CC ProDom; PD007402; Arg_repress; 1.
CC TIGRFAMs; TIGR01529; argR whole; 1.
CC Transcription regulation; DNA-binding; Trans-acting factor; Repressor;
KW Arginine biosynthesis; Complete proteome.
SQ ARGinine biosynthesis; Complete proteome.
SQ SEQUENCE 149 AA; 1681 MW; 364222B56ADDE1BF CRC64;

Query Match 7.0%; Score 6; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 NEIDTQ 54
|||
DQ 17 NEIDTQ 22

RESULT 13
ID ARG_LISMO STANDARD; PRT; 149 AA.
AC Q8V7B9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Arginine repressor.
DE ARG_LISMO OR LM01367.
GN Listeria monocytogenes.
OS Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=16339;
OX [1]
PP SEQUENCE FROM N.A.
RC STRAIN=EGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=1679669;
RA Glaeser P., Frangoul L., Buchrieser C., Ruenliok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbat A., Chetoui F., Couve E., de Daruvar A., Denoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fahli H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Mediari H.,
RA Nordstedt G., Novella S., de Pablo B., Perez-Baz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of *Listeria* species.";
RL Science 294:849-852(2001).
CC -!- FUNCTION: Regulates arginine biosynthesis genes (By similarity).
CC -!- PATHWAY: Arginine biosynthesis; regulation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the argR family.
CC
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CC -----
 DR EMBL; AL591978; CAC99445.1; -;
 DR PIR; AG1245; AG1245.
 DR ListList; LMO01367; -;
 DR HAMAP; MF_00173; -; 1.
 DR InterPro; IPR001669; Arg_repress.
 DR Pfam; PF01316; Arg_repressor; 1.
 DR Pfam; PF02863; Arg_repressor; 1.
 DR PRINTS; PR01467; ARGREPRESSOR.
 DR ProDom; PD007402; Arg_repress; 1.
 DR TrGFams; TIGR01529; argR_whole; 1.
 KW Transcription regulation; DNA-binding; Trans-acting factor; Repressor;
 KW Arginine biosynthesis; Complete proteome.
 SQ ARGinine biosynthesis; Complete proteome.
 SQ SEQUENCE 149 AA; 16778 MW; 25622476E092E1A1 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 149;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 NEIDTQ 54
 Db 17 NEIDTQ 22

RESULT 14
 YBE6 PSEAE
 ID YBE6 PSEAE STANDARD; PRT; 152 AA.
 AC QSHV53;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical UPF0090 protein PA4746.
 GN PA4746.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OC NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goulet S., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen";
 RL Nature 406:959-964 (2000).
 CC -1- SIMILARITY: Belongs to the UPF0090 family.

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CC -----
 DR EMBL; A8004888; AAC08132.1; -;
 DR PIR; A83053; A83053.
 DR HAMAP; MF_01077; -; 1.
 DR InterPro; IPR003728; DUF150.
 DR Pfam; PF02576; DUF150; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 152 AA; 17171 MW; 22583E3104CB50AD CRC64;

Query Match 7.0%; Score 6; DB 1; Length 152;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 QVSGIL 37
 Db 58 QVSGIL 63

RESULT 15
 YGAO BACSU
 ID YGAO BACSU STANDARD; PRT; 157 AA.
 AC P97029;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical lipoprotein ygaO precursor.
 GN YGAO OR BS008890.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Cummings N.J., Ruiz-Teran F., Connerton I.F.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue J., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler H., Wedler H., Weitzenegger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256 (1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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DR EMBL; Z93102; CAB07526.1; -;
 DR EMBL; Z99108; CAB12717.1; -;
 DR PIR; B69817; B69817.
 DR Subtilist; BG12234; YgaO.
 DR InterPro; IPR000437; Prok_lipoprot_5.

DR PROSITE: PS00013; PROKAR LIPOPROTEIN; 1.
 KW Hypothetical protein; Transmembrane; Membrane; Lipoprotein; Signal;
 KW Complete proteome; Palmitate.
 FT SIGNAL 1 17 Potential.
 FT CHAIN 18 157 Hypothetical lipoprotein ygaO.
 FT TRANSMEM 42 64 Potential.
 FT TRANSMEM 98 120 Potential.
 FT TRANSMEM 124 146 Potential.
 FT LIPID 18 18 N-palmitoyl cysteine (Potential).
 FT LIPID 18 18 S-diacylglycerol cysteine (Potential).
 SQ SEQUENCE 157 AA; 17773 MW; F896AE181D784DDB CRC64;

Query Match 7.0%; Score 6; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DEREQM 7

Db 85 DEREQM 90

RESULT 16
 YE56 HAEIN STANDARD; PRT; 168 AA.
 AC P44203;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein H11456.
 GN H11456.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=RD / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA Kennedy K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
 RL Science 269:496-512(1995).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U32823; AAC23106.1; -;
 CC DR PIR; F64030; F64030.
 CC DR TIGR; H11456; -;
 CC KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 23 47 POTENTIAL.
 SQ SEQUENCE 168 AA; 18751 MW; 1A86077999148E9A CRC64;

Query Match 7.0%; Score 6; DB 1; Length 168;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 NLEQVS 34

Db 146 NLEQVS 151

RESULT 17
 ATPF CHLRE STANDARD; PRT; 175 AA.
 AC Q8HTL5; Q9T2G6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE ATP synthase B chain (EC 3.6.3.14) (Subunit 1).
 GN ATPF.
 OS Chlamydomonas reinhardtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rivier C., Rahire M., Rochaix J.-D.;
 RT "Chlamydomonas reinhardtii chloroplast atpF gene."
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 13-31.
 RC STRAIN=cw15;
 RX MEDLINE=96128220; PubMed=8543042;
 RA Fiedler H.R., Schmid R., Leu S., Shavit N., Strotmann H.;
 RT "Isolation of CFOCF1 from Chlamydomonas reinhardtii cw15 and the N-
 RT terminal amino acid sequences of the CFOCF1 subunits."
 RL FEBS Lett. 377:163-166(1995).
 RN [3]
 RP COMPLETE PLASTID GENOME.
 RX MEDLINE=22305394; PubMed=12417694;
 RA Maul J.E., Lilly J.W., Cui L., dePamphilis C.W., Miller W.,
 RA Harris E.H., Stern D.B.;
 RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
 RT a sea of repeats."
 RL Plant Cell 14:2659-2679(2002).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
 CC core - and CF(0) - the membrane proton channel. CF(1) has five
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
 CC has three main subunits: a, b and c.
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
 CC -!- SIMILARITY: Belongs to the ATPase B chain family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AY161319; AA041265.1; ALT INIT.
 CC DR EMBL; BK000554; DAA00955.1; ALT INIT.
 CC DR InterPro: IPR002146; ATPsynt B/E/sub.
 CC DR Pfam: PF00430; ATP-synt B.1
 CC KW Hydrogen ion transport; Transmembrane; CF(0); Chloroplast.
 FT TRANSMEM 20 42 POTENTIAL.
 FT CONFLICT 13 13 H -> M (IN REF. 2).
 FT CONFLICT 31 31 A -> Y (IN REF. 2).
 SQ SEQUENCE 175 AA; 20064 MW; F0FB3D5195C19B34 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EAMORA 79

Db 62 EAMORA 67

"The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hypervariable sequences." ;

RL Nature 403:665-668 (2000).

CC -/- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-riboseyl)-anthranilate = 1-(2-carboxyphenylamino)-1-deoxy-D-ribose 5-phosphate.

CC -/- PATHWAY: Tryptophan biosynthesis; third step.

CC -/- SIMILARITY: Belongs to the trpF family.

CC

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CC

CC EMBL; ALI39075; CAB74184.1; -.

DR PIR; B81377; B81377.

DR HSP; Q56320; 1DL3.

DR HAMAP; MF 00135; -; 1.

DR InterPro; IPR001240; PRA1.

DR Pfam; PF00697; PRA1; 1.

DR Isomerase; Tryptophan biosynthesis; Complete proteome.

CC SQ SEQUENCE 195 AA; 22481 MW; ACBE754AD6E4B877 CRC64 ;

CC

Query Match 7.0%; Score 6; DB 1; Length 199;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 DENLEQ 32

|||||

DB 62 DENLEQ 67

RESULT 20

YE15_HAEIN

ID YE15_HAEIN STANDARD; PRT; 200 AA.

AC P44187;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypothetical protein H11415.

GN H11415.

OS Haemophilus influenzae.

OS Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;

OS Pasteurellaceae; Haemophilus.

OC NCBI_TaxID=727;

CC [1]

RP SEQUENCE FROM N.A.

RC STRAIN=rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;

RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerkvagne A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,

RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georghagen N.S.M.,

RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

RA Venter J.C.;

CC "Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd."

CC

CC -/- SIMILARITY: SOME, TO MYCOBACTERIOPHAGES D29 AND L5 GP10.

CC

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CC

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DR EMBL; U32821; AAC23066.1; -.
DR PIR; H64028; H64028.
DR HSP; P23951; 2BAA.
DR TIGR; H1415; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 200 AA; 22895 MW; 42199FDDA4859FBB CRC64;

Query Match 7.0%; Score 6; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 SGGFIR 15
DB 51 SGGFIR 56

RESULT 21
CERL HUMAN
ID CERL HUMAN STANDARD; PRT; 201 AA.
AC QNTU7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cerebellin-like glycoprotein 1 precursor.
GN CELNL1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
MEDLINE-21638749; PubMed-11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivaeslatho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.M., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sing S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SIMILARITY: Contains 1 Clq domain.
CC
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CC
CC EMBL; AL117383; CAB90173.1; -.
CC Genew; HGNC:16231; CBLNL1.
CC InterPro; IPR001073; Clq.
CC InterPro; IPR008983; TNF_like.

```

Query Match 7.0%; Score 6; DB 1; Length 201;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIM 62
 DB 187 QIDRIM 192

RESULT 23
 MTRD METKA
 ID MTRD METKA STANDARD; PRT; 225 AA.
 AC Q32864;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tetrahydromethanopterin S-methyltransferase subunit D (EC 2.1.1.86)
 DE (N5-methyltetrahydromethanopterin--coenzyme M methyltransferase subunit D).
 DE MTRD OR MK0657.
 GN Methanopyrus kandleri.
 OS Methanopyrus kandleri.
 OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
 OC Methanopyrus.
 OC NCBI_TaxID=2320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98121200; PubMed=9461302;
 RA Harms U., Thauer R.K.;
 RT "Identification of the active site histidine in the corrinoid protein MtrA of the energy-conserving methyltransferase complex from Methanobacterium thermoautotrophicum.";
 RL Eur. J. Biochem. 250:783-788(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AV19 / DSM 6324 / JCM 9639;
 RX MEDLINE=21927647; PubMed=11930014;
 RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N., Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Natale D.A., Rozhin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O., Malykh A.G., Koonin E.V., Kozyavkin S.A.;
 RA "The complete genome of hyperthermophile Methanopyrus kandleri AV19 and monophyly of archaeal methanogens.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
 CC -I- FUNCTION: Part of a complex that catalyzes the formation of methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and methyl-tetrahydromethanopterin. This is an energy-conserving, sodium-ion translocating step (By similarity).
 CC -I- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-mercaptosulfonate = 5,6,7,8-tetrahydromethanopterin + 2-(methylthio)ethanesulfonate.
 CC -I- PATHWAY: Methanogenesis from carbon dioxide; sixth step.
 CC -I- SUBUNIT: The complex is composed of 8 subunits; mtrA, mtrB, mtrC, mtrD, mtrE, mtrF, mtrG and mtrH (By similarity).
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -I- SIMILARITY: Belongs to the mtrD family.

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EMBL; Y14428; CAA74768.1; -;
 DR EMBL; AE010359; AA001872.1; -;
 DR HAMAP; MF 01097; -; 1.
 DR InterPro; IPR005779; Met_transd.
 DR Pfam; PF04207; MtrD; 1.
 DR TIGRFAMs; TIGR01112; mtrD; 1.
 KW Methanogenesis; One-carbon metabolism; Transferase; Methyltransferase; Transmembrane; Complete proteome.
 FT TRANSMEM 5 25
 POTENTIAL.

FT TRANSMEM 40 60
 FT TRANSMEM 67 87
 FT TRANSMEM 132 152
 FT TRANSMEM 161 181
 FT TRANSMEM 204 224
 SQ SEQUENCE 225 AA; 22872 MW; 6FA9546897670D36 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 225;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 VSGILG 38
 DB 135 VSGILG 140

RESULT 24
 YIW2 YEAST
 ID YIW2 YEAST STANDARD; PRT; 236 AA.
 AC P40586;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical 27.4 kDa protein in HYR1 3' region.
 GN YIR042C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OC NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=8288c / AB972;
 RX MEDLINE=97313266; PubMed=9169870;
 RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N., Harris D.E., Hortsell T., Hunt S., Jagels K., Jones M., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N., Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.;
 RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
 RL Nature 387:84-87(1997).
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EMBL; Z46902; CAA87001.1; -;
 DR PIR; S50347; S50347.
 DR GeneOnline; 139754; -;
 DR SGD; S0001481; YIR042C.
 DR InterPro; IPR000182; GCN5acetyl_trans.
 DR Pfam; PF00583; Acetyltransf; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 27422 MW; 1B33E72F8B7AB1C6 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 236;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEAN 76
 DB 108 RIDEAN 113

RESULT 25
 KESC RAT
 ID KESC RAT STANDARD; PRT; 238 AA.
 AC P56536;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific
2) (fragment).
GN KIF5C OR NKHC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC TISSUE=Brain;
RX MEDLINE=98070240; PubMed=9405049;
RA Sack S., Mueller J., Marx A., Thormaehlen M., Mandelkow E.M.,
Brady S.T., Mandelkow E.;
RT "X-ray structure of motor and neck domains from rat brain kinesin.";
RL Biochemistry 36:16155-16165(1997).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).
RX MEDLINE=98088797; PubMed=9428521;
RA Kozielewski F., Sack S., Marx A., Thormaehlen M., Schonbrunn E., Biou V.,
Thompson A., Mandelkow E.M., Mandelkow E.;
RT "The crystal structure of dimeric kinesin and implications for
microtubule-dependent motility.";
RL Cell 91:985-994(1997).
CC -1- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -1- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -1- DOMAIN: Composed of three structural domains: a large globular N-
CC terminal domain which is responsible for the motor activity of
CC kinesin (it hydrolyzes ATP and binds microtubule), a central
CC alpha-helical coiled coil domain that mediates the heavy chain
CC dimerization; and a small globular C-terminal domain which
CC interacts with other proteins (such as the kinesin light chains),
CC vesicles and membranous organelles.
CC -1- SIMILARITY: Belongs to the kinesin-like protein family. Kinesin
CC subfamily.
DR PDB; 2KIN; 08-APR-98.
DR PDB; 3KIN; 14-OCT-98.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS0067; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubule; ATP-binding; Coiled coil; 3D-structure.
FT INIT_MET 0 0
FT DOMAIN 1 1 >238 KINESIN-MOTOR (BY SIMILARITY).
FT NP_BIND 173 >238 MICROTUBULE-BINDING.
FT STRAND 85 92 ATP (BY SIMILARITY).
FT STRAND 4 7
FT HELIX 9 14
FT TURN 19 23
FT TURN 24 25
FT STRAND 28 28
FT TURN 30 33
FT TURN 34 36
FT STRAND 37 40
FT TURN 41 42
FT STRAND 46 47
FT STRAND 50 52
FT TURN 54 55
FT HELIX 58 65
FT TURN 66 66
FT TURN 67 74
FT TURN 75 76
FT STRAND 78 84
FT TURN 87 88
FT HELIX 91 95
FT TURN 96 96
FT TURN 97 97
FT STRAND 99 100
FT TURN 102 104

FT STRAND 105 105
FT HELIX 107 120
FT TURN 121 121
FT TURN 124 125
FT STRAND 126 138
FT TURN 139 140
FT STRAND 141 144
FT TURN 145 146
FT TURN 148 149
FT STRAND 153 153
FT STRAND 157 157
FT TURN 159 160
FT STRAND 163 165
FT TURN 166 167
FT STRAND 171 173
FT HELIX 176 191
FT TURN 192 193
FT HELIX 197 203
FT STRAND 205 216
FT TURN 217 219
FT STRAND 222 231
FT STRAND 237 238
FT NON_TER 238 238
SQ SEQUENCE 238 AA; 27034 MW; 7B254F4894E3BC30 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 238;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY ' 26 MDENLE 31
DB ' 122 MDENLE 127
RESULT 26
YZ2T_AGRVI
ID YZ2T_AGRVI STANDARD; PRT; 242 AA.
AC O34299;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in TAR-II TTUC' 3'region (ORF22) (Fragment).
OS Agrobacterium vitis (Rhizobium vitis).
OG Plasmid pTIAB3.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=373;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB3;
RA Salomone J.-Y., Crouzet P., de Ruffray P., Otten L.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO A.VITIS HYPOTHETICAL 52.8 kDa PROTEIN IN TAR-I
CC TTUC' 3'REGION (AC P70795).
CC
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CC
CC EMBL; AF010415; AAB67102.1; -.
DR InterPro; IPR002823; DUF112.
DR Pfam; PF01970; DUF112; 1.
KW Hypothetical protein; Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 242 AA; 25516 MW; 02324E1DACB81B07 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 242;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 VSGILG 38
 DB 159 VSGILG 164

RESULT 27

KDSB_FUSNN STANDARD; PRT; 245 AA.
 AC QSRPAB;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) (CMP-KDO
 synthetase) (CMP-2-keto-3-deoxyoctulosonic acid synthetase) (CKS).
 GN KDSB OR FN0807.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]_TaxID=76856;
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=1189109;
 RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Foustain M., Kyridides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 CC -!- FUNCTION: Activates KDO (a required 8-carbon sugar) for
 incorporation into bacterial lipopolysaccharide in Gram-negative
 bacteria (by similarity).
 CC -!- CATALYTIC ACTIVITY: CTP + 3-deoxy-D-manno-octulosonate =
 CTP diphosphate + CMP-3-deoxy-D-manno-octulosonate.
 CC -!- PATHWAY: Lipopolysaccharide biosynthesis.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -!- SIMILARITY: Belongs to the KdsB family.
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 CC
 CC EMBL; A010590; AAL95003.1; -.
 CC HAMAP; MF 00057; -; 1.
 CC InterPro; IPR003329; Cytidylyl_trans.
 CC InterPro; IPR004528; KdsB.
 CC Pfam; PF02348; CTP_transf_3; 1.
 CC TIGRFAMs; TIGR00466; kdsB; 1.
 CC Lipopolysaccharide biosynthesis; Transferase; Nucleotidyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 245 AA; 28426 MW; C57AFD7227790D98 CRC64;
 Query Match 7.0%; Score 6; DB 1; Length 245;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ENLRQV 33
 DB 229 ENLRQV 234

RESULT 28

RPIA_TREPA STANDARD; PRT; 254 AA.
 AC Q83625;
 DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ribose 5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)
 DE (PPI).
 GN RPIA OR TP0616.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]_TaxID=160;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
 RA McDonald L., Attiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete".
 RL Science 281:375-388(1998).
 CC -!- CATALYTIC ACTIVITY: D-ribose 5-phosphate = D-ribulose 5-phosphate.
 CC -!- PATHWAY: Nonoxidative branch of the pentose phosphate pathway.
 CC -!- SIMILARITY: Belongs to the ribose 5-phosphate isomerase family.
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 CC
 CC EMBL; AF001236; AAC65592.1; -.
 CC PIR; E71303; E71303.
 CC TIGR; TP0616; -.
 CC HAMAP; MF 00170; -; 1.
 CC InterPro; IPR004788; RpiA.
 CC ProDom; PD005813; RpiA; 1.
 CC TIGRFAMs; TIGR00021; rpiA; 1.
 CC Isomerase; Complete proteome.
 KW Isomerase; Complete proteome.
 SQ SEQUENCE 254 AA; 27572 MW; 028FACD2FC5F3751 CRC64;
 Query Match 7.0%; Score 6; DB 1; Length 254;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 EIDTQN 55
 DB 109 EIDTQN 114

RESULT 29
 YRKJ_BACSU STANDARD; PRT; 261 AA.
 AC P54437;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical protein yrkU.
 GN YRKJ OR BSU26490.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=97124195; PubMed=8969508;
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
 RA Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 the Bacillus subtilis genome containing the skin element and many

RT sporulation genes";
 RL Microbiology 142:3103-3111 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogatawara N., Mozer L., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Erington J., Fabbet C., Ferrari E., Poulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.F., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpträ P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa K., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis".
 RL Nature 390:249-256 (1997).
 RL Nature 390:249-256 (1997).
 CC -1- SURCELLULAR LOCATION: Integral membrane protein (Potential).
 CC
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 CC EMBL; D84432; BAB12365.1; -;
 CC EMBL; Z99117; CAB14590.1; -;
 CC PIR; H69976; H69976.
 CC Subtilist; BG11776; yrk.
 CC InterPro; IPR002781; DUF81.
 CC Pfam; PF01925; DUF81; 1.
 CC KW Hypothetical protein; Transmembrane; Complete proteome.
 CC FT TRANSMEM 10 30 POTENTIAL.
 CC FT TRANSMEM 51 71 POTENTIAL.
 CC FT TRANSMEM 80 100 POTENTIAL.
 CC FT TRANSMEM 106 126 POTENTIAL.
 CC FT TRANSMEM 151 171 POTENTIAL.
 CC FT TRANSMEM 186 206 POTENTIAL.
 CC FT TRANSMEM 210 230 POTENTIAL.
 CC FT TRANSMEM 240 260 POTENTIAL.
 CC SEQUENCE 261 AA; 27567 MW; 657367CFC84993B7 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 261;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 VSGILG 38
 |||||
 Db 158 VSGILG 163

RESULT 30
 SET_DROME
 ID SET_DROME STANDARD; PRT; 269 AA.
 AC P53997; Q9VFA5;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SET protein.
 GN SET OR G4299.
 OS Drosophila melanogaster (Fruit fly).
 OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95348188; PubMed=7625566;
 RX Kellogg D.R., Kikuchi A., Fugii-Nakata T., Turck C.W., Murray A.W.;
 RA "Members of the NAP/SET family of proteins interact specifically with
 RT B-type cyclins".
 RL J. Cell Biol. 130:661-673 (1995).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Chen B.D.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballow R.M., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadenot L.B., Davies P.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod W.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster".
 RL Science 287:2185-2195 (2000).
 CC -1- SUBUNIT: Interacts specifically with B-type cyclins.
 CC
 CC -1- SIMILARITY: Belongs to the nucleosome assembly protein (NAP)
 CC family.
 CC
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CC -----
CC EMBL: U30470; AAA74264.1; -.
CC DR EMBL: AE003708; AAF55155.1; -.
CC DR FlyBase; FBN0014879; Set.
CC DR InterPro; IPR002164; NAP_family.
CC DR Pfam; PF00956; NAP; 1.
CC FT DOMAIN 230 269 ASP/GLU-RICH (HIGHLY ACIDIC).
CC FT CONFLICT 15 15 MISSING (IN REF. 1).
CC SQ SEQUENCE 269 AA; 30994 MW; 05F88CB85933BB09 CRC64;

Query Match
Best Local Similarity 7.0%; Score 6; DB 1; Length 269;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
Db 92 QVSGIL 97

RESULT 31
ATBP STRAU STANDARD; PRT; 271 AA.
AC F18179;
ID ATBP STRAU STANDARD; PRT; 271 AA.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Potential ATP-binding protein (ORF 271).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RX SEQUENCE FROM N.A.
RC STRAIN=NCTC 9789; TRANSPOSON=Tn552;
RX MEDLINE=91014696; PubMed=2170815;
RA Rowland S.J., Dyke K.G.H.;
RT "Tn552, a novel transposable element from Staphylococcus aureus.";
RL Mol. Microbiol. 4:961-975(1990).
CC -----
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CC -----
CC EMBL: X52734; CAA36948.1; -.
CC DR FIR; S11779; S11779.
CC KW Transposable element; ATP-binding.
CC FT NP BIND 34 41 ATP (BY SIMILARITY).
CC SQ SEQUENCE 271 AA; 31835 MW; 32F6CCEA73911927 CRC64;

Query Match
Best Local Similarity 7.0%; Score 6; DB 1; Length 271;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 QIDRIM 62
Db 241 QIDRIM 246

RESULT 32
CTX3 HUMAN STANDARD; PRT; 280 AA.
ID CTX3 HUMAN STANDARD; PRT; 280 AA.
AC Q9UQI1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein C20orf103 precursor.
GN C20ORF103.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Stavrides G.S., Huckle E.J., Deloukas P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Jones M., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gillman R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leheslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Strue C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Tishiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madao A., Rodriguez S., Sanchez A.,
RA Whiting M., Madao A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -----
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CC -----
CC EMBL: AL121740; CAB57330.1; -.
CC DR EMBL: AL031652; CAC18101.1; -.
CC DR EMBL: BC050727; AAH50727.1; -.

```

DR Genew: HGNC:16097; C20orf103.
 KW Transmembrane; Signal; Polymorphism.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 280
 FT DOMAIN 30 235
 FT TRANSMEM 236 256
 FT TRANSMEM 236 256
 FT TRANSMEM 236 256
 FT TRANSMEM 236 256
 FT CARBOHYD 35 35
 FT CARBOHYD 53 53
 FT CARBOHYD 127 127
 FT VARIANT 12 12
 FT VARIANT 81 81
 FT VARIANT 103 103
 FT VARIANT 158 158
 FT VARIANT 158 158
 FT SEQUENCE 280 AA; 31472 MW; 7D811D7C04EE70B8 CRC64;
 Query Match 7.0%; Score 6; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VDREQ 6
 Db 227 VDREQ 232
 RESULT 33
 ID PSTA_METJA STANDARD; PRT; 281 AA.
 AC Q58419;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable phosphate transport system permease protein pstA.
 GN PSTA OR MJ1013.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=6688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -!- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the binding-protein-dependent transport
 CC system permease family. CysTg subfamily.
 CC -----
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 CC -----
 CC DR EMBL; U67544; AAB99017.1; -.

DR PIR: D64426; D64426.
 DR TIGR: MJ1013;...
 DR InterPro: IPR00515; BPD_transp.
 DR InterPro: IPR005672; Phosp_transpt2.
 DR Pfam: PF00528; BPD_transp; 1.
 DR TIGRFAMs: TIGR00974; 3a0107s02c; 1.
 DR PROSITE: PS00928; ABC_TM1; 1.
 KW Transport; Phosphate Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 16 36 POTENTIAL.
 FT TRANSMEM 68 88 POTENTIAL.
 FT TRANSMEM 107 127 POTENTIAL.
 FT TRANSMEM 128 148 POTENTIAL.
 FT TRANSMEM 194 214 POTENTIAL.
 FT TRANSMEM 251 271 POTENTIAL.
 FT SEQUENCE 281 AA; 30248 MW; A807ECBD406DD45E CRC64;
 Query Match 7.0%; Score 6; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 78 RATKML 83
 Db 103 RATKML 108
 RESULT 34
 ID RS3_HALNI STANDARD; PRT; 302 AA.
 AC P15009; O24784; Q9HPC8;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 20S ribosomal protein S3P (HSA) (HSA83).
 GN RPS3P OR VNG1697G.
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091, 2242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1;
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorason V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., GOO Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Dale H.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Spudich J.L., Jung K.-H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Omer A.D.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=H.halobium;
 RX MEDLINE=89248673; PubMed=2470481;
 RA Spiridonova V.A., Akhmanova A.S., Kagramanova V.K., Koepke A.K.E.,
 RA Mankin A.S.;
 RT "Ribosomal protein gene cluster of Halobacterium halobium: nucleotide
 RT sequence of the genes coding for S3 and L29 equivalent ribosomal
 RT proteins.";
 RL Can. J. Microbiol. 35:153-159(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=H.halobium;
 RX MEDLINE=97031049; PubMed=8876975;
 RA Miyokawa T., Urayama T., Shimooka K., Itoh T.;
 RT "Organization and nucleotide sequences of ten ribosomal protein genes
 RT from the region equivalent to the S10 operon in the archaeobacterium,
 RT Halobacterium halobium.";
 RL Halobacterium halobium. J. Biol. Chem. 269:1209-1220(1994).
 RN [4]

RP SEQUENCE OF 1-16 FROM N.A.
RC SPECIES=H.halobium;
RX MEDLINE=89211383; PubMed=2651152;
RA Mankin A.S.;
RT "The nucleotide sequence of the genes coding for the S19 and L22
RT equivalent ribosomal proteins from Halobacterium halobium.";
RL PERS Lett. 246:13-16(1989).
CC -!- FUNCTION: Binds the lower part of the 30S subunit head (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB005077; AAG19942.1; -.
CC EMBL; X14967; CA33093.1; -.
CC EMBL; AB006961; BAA22276.1; -.
CC PIR; B84322; B84322.
CC PIR; T43822; T43822.
CC HAMAP; MF_01309; -; 1.
CC InterPro; IPR004087; KH dom.
CC InterPro; IPR009019; KH prot.
CC InterPro; IPR004044; KH TYPE 2.
CC InterPro; IPR001351; Ribosomal S3 C.
CC InterPro; IPR005703; S3_euk_arch.
CC Pfam; PF00013; KH; 1.
CC Pfam; PF00189; Ribosomal S3_C; 1.
CC SMART; SM00322; KH; 1.
CC TIGRFAMs; TIGR01008; tpsC_E_A; 1.
CC PROSITE; PS50823; KH TYPE 2; 1.
CC PROSITE; PS00548; RIBOSOMAL_S3; 1.
CC Ribosomal protein; RNA-binding; Complete proteome.
CC DOMAIN 17 86 KH TYPE-2.
CC CONFLICT 32 32 G -> S (IN REF. 2).
CC SEQUENCE 302 AA; 33071 MW; 4AD9D430EA4104B CRC64;
CC -----
CC Query Match 7.0%; Score 6; DB 1; Length 302;
CC Best Local Similarity 100.0%; Pred. No. 61;
CC Matches 6; Conservative 0; Mismatches 0; Gaps 0;
CC -----
CC QY 58 IDIRIME 63
CC Db 117 IDIRIME 122
CC -----
CC RESULT 35
CC RS3 HALMA STANDARD; PRT; 304 AA.
CC AC P20261;
CC DT 01-FEB-1991 (Rel. 17, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE 30S ribosomal protein S3P (HmaS3) (HS1).
CC GN RPS3P.
CC OS Haloarcula marismortui (Halobacterium marismortui).
CC OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
CC OC Halobacteriaceae; Haloarcula.
CC OK NCBI_TaxID=2238;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=90153945; PubMed=2406244;
CC RA Arndt E., Kroemer W., Hatakeyama T.;
CC RT "Organization and nucleotide sequence of a gene cluster coding for
CC eight ribosomal proteins in the archaeobacterium Halobacterium
CC marismortui.";
CC RT J. Biol. Chem. 265:3034-3039(1990).
CC RL

-!- FUNCTION: Binds the lower part of the 30S subunit head (By
CC similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
CC -!- SIMILARITY: Belongs to the S3P family of ribosomal proteins.
CC -!- SIMILARITY: Contains 1 KH type-2 domain.
CC -----
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CC -----
CC EMBL; J05222; AAA86865.1; -.
CC PIR; I35063; R3HS39.
CC HAMAP; MF_01309; -; 1.
CC InterPro; IPR004087; KH dom.
CC InterPro; IPR009019; KH prot.
CC InterPro; IPR004044; KH TYPE 2.
CC InterPro; IPR001351; Ribosomal S3 C.
CC InterPro; IPR005703; S3_euk_arch.
CC Pfam; PF00013; KH; 1.
CC Pfam; PF00189; Ribosomal S3_C; 1.
CC SMART; SM00322; KH; 1.
CC TIGRFAMs; TIGR01008; tpsC_E_A; 1.
CC PROSITE; PS50823; KH TYPE 2; 1.
CC PROSITE; PS00548; RIBOSOMAL_S3; 1.
CC Ribosomal protein; RNA-binding; rRNA-binding.
CC FT DOMAIN 17 86 KH TYPE-2.
CC SQ SEQUENCE 304 AA; 33588 MW; 3E28F3C4548E6F5 CRC64;
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CC Query Match 7.0%; Score 6; DB 1; Length 304;
CC Best Local Similarity 100.0%; Pred. No. 62;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC QY 58 IDIRIME 63
CC Db 117 IDIRIME 122
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CC RESULT 36
CC E2BA HUMAN STANDARD; PRT; 305 AA.
CC AC Q14232;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP
CC exchange factor).
CC GN E2B1 OR EIF2BA.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OK NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Torp A.;
CC RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC RN [2]
CC RP VARIANT VWM TYR-208.
CC RX MEDLINE=21823281; PubMed=11835386;
CC RA van der Knaap M.S., Leegwater P.A.J., Koenst A.A.M., Visser A.,
CC Naidu S., Oudejans C.B.M., Schutgens R.B.H., Pronk J.C.;
CC "Mutations in each of the five subunits of translation initiation
CC factor eIF2B can cause leukoencephalopathy with vanishing white
CC matter.";
CC RT Ann. Neurol. 51:264-270(2002).
CC RL Ann. Neurol. 51:264-270(2002).
CC CC -!- FUNCTION: Catalyzes the exchange of eukaryotic initiation factor
CC 2-bound GDP for GTP.
CC CC -!- SUBUNIT: Complex of five different subunits; alpha, beta, gamma,
CC delta and epsilon.
CC CC -!- DISEASE: Defects in EIF2B1 are a cause of leukoencephalopathy with

CC vanishing white matter (VWM) [MIM:603896]. VWM is a brain disease
 CC that occurs mainly in children. The neurological signs of VWM
 CC include progressive cerebellar ataxia, spasticity, inconstant
 CC optic atrophy and relatively preserved mental abilities. The
 CC disease is chronic-progressive with, in most individuals,
 CC additional episodes of rapid deterioration following febrile
 CC infections or minor head trauma. Head trauma leads only to motor
 CC deterioration, whereas infections with fever may end in coma.
 CC Death occurs after a variable period of a few years to a few
 CC decades, usually following an episode of fever and coma.
 CC -!- SIMILARITY: Belongs to the EIF-2B alpha/beta/delta subunits
 CC family.
 CC
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 CC
 CC EMBL; X95648; CAA64950.1; -
 CC GenBank; HGNC:3257; E1F2B1.
 CC GI; 14232; -
 CC MIM; 606886; -
 CC MIM; 603896; -
 CC GO; GO:0008135; Translation factor activity, nucleic acid b. . . TAS.
 CC InterPro; IPR000649; IF-2B.
 CC Pfam; PF01008; IF-2B; 1.
 CC Initiation factor; Protein biosynthesis.
 CC VARIANT 208 N -> Y (in VWM).
 CC /FTID=VAR 015404.
 CC FT SEQUENCE 305 AA; 33712 MW; 91A915FF1B80B780 CRC64;
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 CC Query Match 7.0%; Score 6; DB 1; Length 305;
 CC Best Local Similarity 100.0%; Pred. No. 62;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 61 IMEXAD 66
 CC | | | | |
 CC Db 186 IMEXAD 191
 CC
 CC RESULT 37
 CC E2B8 MOUSE
 CC ID E2B8 MOUSE STANDARD; PRT; 305 AA.
 CC AC G91LC8;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP
 CC exchange factor).
 CC GN EIF2B1.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=22389257; PubMed=12477932;
 CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 CC Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield F.S.N., Krzywinski M.I., Skalski U., Smalios D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Catalyzes the exchange of eukaryotic initiation factor
 CC 2-bound GDP for GTP
 CC -!- SUBUNIT: Complex of five different subunits; alpha, beta, gamma,
 CC delta and epsilon.
 CC -!- SIMILARITY: Belongs to the EIF-2B alpha/beta/delta subunits
 CC family.
 CC
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 CC
 CC EMBL; BC003426; AAH03426.1; -
 CC MGD; MGI:2384802; E1f2b1.
 CC InterPro; IPR000649; IF-2B.
 CC Pfam; PF01008; IF-2B; 1.
 CC Initiation factor; Protein biosynthesis.
 CC SEQUENCE 305 AA; 33816 MW; 3D9ED81F0D9B8411 CRC64;
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 CC Query Match 7.0%; Score 6; DB 1; Length 305;
 CC Best Local Similarity 100.0%; Pred. No. 62;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 61 IMEXAD 66
 CC | | | | |
 CC Db 186 IMEXAD 191
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 CC RESULT 38
 CC GCP MYCGE
 CC ID GCP MYCGE STANDARD; PRT; 315 AA.
 CC AC P47292;
 CC DT 01-FEB-1996 (Rel. 33, Created)
 CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57).
 CC DE (Glycoprotease).
 CC GN GCP OR MG046.
 CC OS Mycoplasma genitalium.
 CC OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 CC OX NCBI_TaxID=2097;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=ATCC 33530 / G-37;
 CC RX MEDLINE=96026346; PubMed=7569993;
 CC RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 CC Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 CC Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
 CC Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 CC Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
 CC Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
 CC "The minimal gene complement of Mycoplasma genitalium.";
 CC Science 270:397-403(1995).
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of O-sialoglycoproteins; cleaves
 CC 3i-Arg-|-Asp-32 bond in glycoprotein A. Does not cleave
 CC unglycosylated proteins, desialylated glycoproteins or
 CC glycoproteins that are only N-glycosylated.
 CC -!- COFACTOR: Zinc (Probable).
 CC -!- SIMILARITY: Belongs to peptidase family M22.
 CC
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CC -----
 DR EMBL; U39684; RAC71262.1; --
 DR FIR; A64205; A64205.
 DR MEROPS; M22.UPW; --
 DR TIGR; MG046; --
 DR InterPro; IPR000905; Peptidase M22.
 DR Pfam; PF00814; Peptidase M22; 1
 DR PIRSF; PIRSF004537; OsaIglc_Ppids; 1.
 DR PRINTS; PR00789; OSIALOPTASE.
 DR ProDom; PD002367; Peptidase M22; 1.
 DR TIGRFAMs; TIGR00329; gcp; 1.
 DR PROSITE; PS01016; GLYCOPROTEASE; 1.
 KW Hydrolase, Metalloprotease, Zinc; Complete proteome.
 FT METAL 110 110 ZINC (POTENTIAL).
 FT METAL 114 114 ZINC (POTENTIAL).
 SQ SEQUENCE 315 AA; 34708 MW; D186BCD176C4E574 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 315;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 NKTRID 73

|||||

Db 227 NKTRID 232

RESULT 39

PDR BURCE

ID PDR BURCE STANDARD; PRT; 321 AA.

AC P33164; Q9ZFR3;

DT 01-OCT-1993 (Rel. 27, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Phthalate dioxygenase reductase (EC 1.-.-.-) (PDR).

GN OPHAL.

OS Burkholderia cepacia (Pseudomonas cepacia).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_taxid=292;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=DB01;

RX MEDLINE=99069326; PubMed=9851995;

RA Chang H.K., Zylstra G.J.;

RT "Novel organization of the genes for phthalate degradation from

Burkholderia cepacia DB01.";

RL J. Bacteriol. 180:6529-6537(1998).

RN [2]

X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND PARTIAL SEQUENCE.

RC STRAIN=DB01;

RX MEDLINE=93088078; PubMed=1280857;

RA Correll C.C., Balle C.J., Ballou D.P., Ludwig M.L.;

RT "Phthalate dioxygenase reductase: a modular structure for electron

transfer from pyridine nucleotides to [2Fe-2S].";

RL Science 258:1604-1610(1992).

CC -|- FUNCTION: COMPONENT OF THE ELECTRON TRANSFER CHAIN INVOLVED IN

PYRIDINE NUCLEOTIDE-DEPENDENT DIHYDROXYLATION OF PHTHALATE.

CC UTILIZES FMN TO MEDIATE ELECTRON TRANSFER FROM THE TWO-ELECTRON

DONOR, NADH, TO THE ONE-ELECTRON ACCEPTOR, (2Fe-2S).

CC -|- COFACTOR: FMN.

CC -|- SUBUNIT: Monomer.

CC -|- SIMILARITY: Belongs to the pdr/vanB family.

CC -|- SIMILARITY: In the C-terminal section; belongs to the 2Fe2S plant-

CC type ferredoxin family.

CC -----

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CC EMBL; AF095748; AAD03550.1; --

DR FIR; A44230; A44230.

DR PDB; 2PIA; 15-APR-93.

DR InterPro; IPR006058; 2Fe2S_fd_BS.

DR InterPro; IPR008333; FAD binding_6.

DR InterPro; IPR001041; Ferredoxin.

DR InterPro; IPR001433; Oxred FAD/NAD(P).

DR InterPro; IPR000951; Phdiox_reductase.

DR Pfam; PF00970; FAD_binding_6; 1.

DR Pfam; PF00111; fer2; 1.

DR Pfam; PF00175; NAD binding_1; 1.

DR PRINTS; PR00409; PHDIOXRDTASE.

DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.

KW Oxidoreductase; Flavoprotein; FMN; NAD; Metal-binding; Iron-sulfur;

KW Iron; 2Fe-2S; 3D-structure; Electron transport.

FT INIT MET 0 0

FT NP BIND 1 102 FMN.

FT NP BIND 112 226 NAD.

FT METAL 272 272 IRON-SULFUR (2FE-2S).

FT METAL 277 277 IRON-SULFUR (2FE-2S).

FT METAL 280 280 IRON-SULFUR (2FE-2S).

FT METAL 308 308 IRON-SULFUR (2FE-2S).

FT TURN 3 7

FT STRAND 9 20

FT TURN 21 22

FT STRAND 23 29

FT TURN 31 32

FT TURN 41 42

FT STRAND 44 48

FT TURN 50 51

FT STRAND 54 58

FT TURN 63 64

FT STRAND 68 74

FT TURN 77 78

FT HELIX 82 88

FT TURN 92 93

FT STRAND 95 98

FT TURN 102 102

FT STRAND 109 110

FT TURN 113 119

FT STRAND 120 122

FT HELIX 123 136

FT STRAND 140 147

FT HELIX 150 152

FT TURN 154 155

FT HELIX 156 160

FT TURN 162 167

FT STRAND 168 172

FT TURN 174 175

FT TURN 177 178

FT HELIX 183 187

FT TURN 192 193

FT STRAND 194 199

FT HELIX 202 211

FT TURN 212 214

FT TURN 217 218

FT STRAND 220 223

FT STRAND 238 242

FT TURN 243 245

FT STRAND 248 251

FT TURN 253 254

FT HELIX 257 263

FT TURN 264 265

FT TURN 279 280

FT STRAND 281 286

FT STRAND 289 290

FT TURN 298 303

FT STRAND 304 306


```

FT TURN 307 309
FT STRAND 311 312
FT STRAND 316 319
SQ SEQUENCE 321 AA; 35533 MW; 84E179CED06D85F CRC64;

Query Match 7.0%; Score 6; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TNAREN 23
|||||
Db 230 TNAREN 235

RESULT 40
YC78 SYN3
ID YC78 SYN3 STANDARD; PRT; 330 AA.
AC P74192;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein slr1278.
GN SLR1278.
OS Synchocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nambu K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res 3:109-136(1996).
CC -!- SIMILARITY: BELONGS TO THE UPF0072 (MESI/YCF62) FAMILY.
CC
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CC
CC EMBL; D90913; BAA18281.1; -
CC PIR; S75822; S75822.
CC InterPro; IPR000541; UPF0021.
CC Pfam; PF01171; ATP_bind3; 1.
CC KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 330 AA; 37771 MW; C7672AC09596E723 CRC64;

Query Match 7.0%; Score 6; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
|||||
Db 239 LEQVSG 244

RESULT 41
YA65 METUA
ID YA65 METUA STANDARD; PRT; 337 AA.
AC Q58465;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein MJ1065.
GN MJ1065.

```

```

OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: STRONG, TO B.SUBTILIS SPSE.
CC -!- SIMILARITY: Contains 1 AFP-like domain.
CC
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CC
CC EMBL; U67549; AAB99068.1; -
CC PIR; H64432; H64432.
CC TIGR; MJ1065; -
CC InterPro; IPR006014; Antifreeze dom.
CC InterPro; IPR006190; Antifreeze-like.
CC Pfam; PF01354; Antifreeze; 1.
CC Pfam; PF03102; Neuf; 1.
CC PROSITE; PS05844; AFP LIKE; 1.
CC KW Hypothetical protein; Complete proteome.
FT DOMAIN 279 337 AFP-LIKE.
SQ SEQUENCE 337 AA; 37976 MW; 790CCAF48C111B CRC64;

Query Match 7.0%; Score 6; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 KMLGSG 86
|||||
Db 256 KMLGSG 261

RESULT 42
MURG HAEIN
ID MURG HAEIN STANDARD; PRT; 351 AA.
AC P45065;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide)
DE pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
DE (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc
DE transferase).
GN MURG OR H1138.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

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RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.B., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Wetland J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: Cell wall formation. Catalyzes the transfer of a GlcNAc
CC subunit on undecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid
CC intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc-
CC (pentapeptide)GlcNAc (lipid intermediate II) (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl)-L-Ala-
CC gamma-D-Glu-D-Lys-D-Ala-D-Ala-diphosphoundecaprenol = UDP +
CC GlcNAc-(1->4)-Mur2Ac(oyl)-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-
CC diphosphoundecaprenol.
CC -!- PATHWAY: Peptidoglycan biosynthesis; last step.
CC -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC -!- SIMILARITY: Belongs to the glycosyltransferase family 28. MurG
CC subfamily.
CC
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CC
CC EMBL; U32793; AAC22793.1; -.
CC PIR; D64185; D64185.
CC HSPF; P17443; IF0K.
CC TIGR; H11138; -.
CC HAMAP; MF_00033; -.
CC InterPro; IPR007235; Glyco_tran_28_C.
CC InterPro; IPR004276; Glyco_tran_28.
CC InterPro; IPR006009; MurG..
CC Pfam; PF04101; Glyco_tran_28_C; 1.
CC Pfam; PF03033; Glyco_transf_28; 1.
CC TIGRFAMs; TIGR01133; murG; 1.
CC Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane;
CC Inner membrane; Peptidoglycan synthesis; Complete proteome.
CC SEQUENCE 351 AA; 38307 MW; 410673799B30B27 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 ENLEQV 33
DB 230 ENLEQV 235
RESULT 43
ALR_NEIMA ID - ALR_NEIMA STANDARD; PRT; 352 AA.
AC Q9JTA6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR NMA1906.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagsels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC
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CC
CC EMBL; AL162757; CAB85127.1; -.
CC PIR; B81818; B81818.
CC HSPF; P10724; 1BD0.
CC HAMAP; MF_01201; -.
CC InterPro; IPR000821; Ala_racemase.
CC InterPro; IPR009006; Racem_decarbox_C.
CC InterPro; IPR001608; UPF0001.
CC Pfam; PF00842; Ala_racemase_C; 1.
CC Pfam; PF01168; Ala_racemase_N; 1.
CC PRINTS; PR00992; ALARACEMASE.
CC TIGRFAMs; TIGR00492; alt; 1.
CC Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
CC Complete proteome.
CC ACT_SITE 33 33 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
CC ACT_SITE 250 250 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
CC BINDING 33 33 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 352 AA; 38848 MW; B595D0B0F3D6ADD5 CRC64;
Query Match 7.0%; Score 6; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 LGNLRH 42
DB 10 LGNLRH 15
RESULT 44
ALR_NEIMB ID - ALR_NEIMB STANDARD; PRT; 352 AA.
AC Q9JYC4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR NMB1651.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

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RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citterone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizzi M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815 (2000).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL; AE002515; AAF42000.1; -.
DR F1; B81059; B81059.
DR HSSP; P10724; 1BD0.
DR TIGR; NMB1651; -.
DR HAMAP; MF 01201; -.
DR InterPro; IPR000821; Ala racemase.
DR InterPro; IPR009006; Racem decarbox_C.
DR InterPro; IPR001608; UPP0001.
DR Pfam; PF00842; Ala racemase C; 1.
DR Pfam; PF01168; Ala racemase N; 1.
DR PRINTS; PR00992; ALARACEMASE.
DR TIGRFAMs; TIGR00492; alt; 1.
DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KW Complete proteome.
FT ACT_SITE 33 33 CATALYTIC BASE SPECIFIC TO D-ALANINE (BY
FT ACT_SITE 250 250 SIMILARITY).
FT ACT_SITE 333 333 CATALYTIC BASE SPECIFIC TO L-ALANINE (BY
FT BINDING 33 33 PYRIDOXAL PHOSPHATE (BY SIMILARITY)).
FT BINDING 352 AA; 38820 MW; OAC568A9E1286056 CRC64;
SQ SEQUENCE 352 AA; 7.0%; Score 6; DB 1; Length 352;
Query Match 7.0%; Score 6; DB 1; Length 352;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 LGNLRH 42
DB 10 LGNLRH 15

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RESULT 45

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ALR CHLITE STANDARD; PRT; 383 AA.
AC Q8KB67;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanine racemase (EC 5.1.1.1).
GN ALR OR CT1922.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OK NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TLS / ATCC 49652 / DSM 12025;

```

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RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.J., DeBoy R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Unayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Rettelin H., Bryant D.A., Fraser C.M.; TLS, a
RT "The complete genome sequence of Chlorobium tepidum TLS, a
RT photosynthetic, anaerobic, green-sulfur bacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
CC -!- FUNCTION: Provides the D-alanine required for cell wall
CC biosynthesis (By similarity).
CC -!- CATALYTIC ACTIVITY: L-alanine = D-alanine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; first
CC step.
CC -!- SIMILARITY: Belongs to the alanine racemase family.
CC -----
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CC -----
DR EMBL; AE012943; ANM73141.1; -.
DR TIGR; CT1922; -.
DR HAMAP; MF 01201; -.
DR InterPro; IPR000821; Ala racemase.
DR InterPro; IPR009006; Racem decarbox_C.
DR InterPro; IPR001608; UPP0001.
DR Pfam; PF00842; Ala racemase C; 1.
DR Pfam; PF01168; Ala racemase N; 1.
DR PRINTS; PR00992; ALARACEMASE.
DR TIGRFAMs; TIGR00492; alt; 1.
DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate; Cell wall; Peptidoglycan synthesis;
KW Complete proteome.
FT ACT_SITE 50 50 CATALYTIC BASE SPECIFIC TO D-ALANINE
FT ACT_SITE 279 279 (BY SIMILARITY).
FT ACT_SITE 50 50 CATALYTIC BASE SPECIFIC TO L-ALANINE
FT BINDING 50 50 (BY SIMILARITY).
FT BINDING 383 AA; 40986 MW; B41AF5C33872DEC CRC64;
SQ SEQUENCE 383 AA; 7.0%; Score 6; DB 1; Length 383;
Query Match 7.0%; Score 6; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 LGNLRH 42
DB 25 LGNLRH 30

```

Search completed: March 4, 2004, 08:33:19
Job time : 15 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:31:05 ; Search time 21 Seconds
(without alignments)
393.927 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDEREQALSGFIRRVINA.....SNKTRIDEANQATKMLGSG 86

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	57.0	204	2 150480	synapse protein SN
2	49	57.0	206	2 A37861	synaptosomal-assoc
3	49	57.0	206	2 I53735	nerve terminal pro
4	49	57.0	206	2 I67823	nerve terminal pro
5	49	57.0	206	2 A33623	synaptosomal-assoc
6	27	31.4	249	2 S38308	SNAP-25 protein -
7	27	31.4	249	2 S38309	SNAP-25 protein -
8	25	29.1	203	2 150481	synapse protein SN
9	15	17.4	16	2 A44823	synaptosomal-assoc
10	15	17.4	46	2 S32362	SNAP receptor - bo
11	12	14.0	56	2 S36812	probable synapse-a
12	11	12.8	29	2 A49708	synaptosomal-assoc
13	10	11.6	210	2 150552	synapse protein -
14	10	11.6	210	2 UC5512	SNARE protein 23 -
15	8	9.3	357	2 H89819	conserved hypothet
16	8	9.3	593	2 H64529	hypothetical prote
17	7	8.1	350	2 A97278	mannose-1-phosphat
18	7	8.1	362	2 A33144	conserved hypothet
19	7	8.1	380	2 E30797	hypothetical prote
20	7	8.1	380	2 G85657	hypothetical prote
21	7	8.1	386	2 T19354	hypothetical prote
22	7	8.1	387	2 C86640	multidrug efflux t
23	7	8.1	396	2 C98143	hypothetical prote
24	7	8.1	875	2 T45813	hypothetical prote
25	7	8.1	1643	2 T05647	hypothetical prote
26	7	8.1	1711	2 T06119	hypothetical prote
27	7	8.1	1750	2 E86151	hypothetical prote
28	7	8.1	1793	2 T47897	guanine nucleotide
29	6	7.0	75	2 T42409	PMFamide-like pep

30 6 7.0 84 2 AH3402 hypothetical cytos
31 6 7.0 106 2 T26263 PMFamide-like pep
32 6 7.0 111 2 T40946 60S ribosomal prot
33 6 7.0 118 2 T17380 v1A protein - Dic
34 6 7.0 120 2 D82022 truncated pilin NM
35 6 7.0 124 2 E89984 hypothetical prote
36 6 7.0 127 2 AH3491 hypothetical cytos
37 6 7.0 138 2 T46908 hypothetical prote
38 6 7.0 141 2 T39245 ef-hand protein -
39 6 7.0 143 2 C44259 kinesin heavy chai
40 6 7.0 147 2 S31243 ribosomal protein
41 6 7.0 148 2 G95210 acetyltransferase,
42 6 7.0 148 2 A98075 conserved hypothet
43 6 7.0 149 2 AC1608 arginine repressor
44 6 7.0 149 2 AG1245 arginine repressor
45 6 7.0 152 2 A83053 conserved hypothet

ALIGNMENTS

RESULT 1
150480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50480
R:Kislinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EWBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-204 <RIS>
A:Cross-references: GB:I22973; NID:g349426; PIDN:AAA16537.1; PID:g349427
C:Genetics:
A:Gene: SNAP-25

Query Match 57.0%; Score 49; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDPNQRIQDRIMEKADSNKTRIDEANQATKMLGSG 86
DB 156 GNLRHMDMGNEIDPNQRIQDRIMEKADSNKTRIDEANQATKMLGSG 204

RESULT 2

A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:Catibacas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coinci
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDPNQRIQDRIMEKADSNKTRIDEANQATKMLGSG 86
DB 158 GNLRHMDMGNEIDPNQRIQDRIMEKADSNKTRIDEANQATKMLGSG 206

```
RESULT 3
I53735
C:Species: Homo sapiens - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI19760; NID:g307425; PIDN:AAAC37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
|||||
Db 158 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206

RESULT 4
I67823
C:Species: Homo sapiens - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:LI19761; NID:g307427; PIDN:AAAC37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
|||||
Db 158 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206

RESULT 5
A33623
synaptosomal-associated 25K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998
```

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Query Match 57.0%; Score 49; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
|||||
Db 158 GNLHWMALDNGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206

RESULT 6
S38308
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38308
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38308
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 31.4%; Score 27; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWMALDNGNEIDTQNRQIDRIMEK 64
|||||
Db 158 GNLHWMALDNGNEIDTQNRQIDRIMEK 184

RESULT 7
S38309
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding di
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 31.4%; Score 27; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.2e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLHWMALDNGNEIDTQNRQIDRIMEK 64
|||||
Db 158 GNLHWMALDNGNEIDTQNRQIDRIMEK 184

RESULT 8
I50481
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50481
R:Kislinger, C.; Lathamar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
```

A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50481
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RIS>
A:Cross-references: GB:L22976; NID:G349430; PIDN:AAA16538.1; PID:G349431
C:Genetics:
A:Gene: SNAP-25

Query Match 29.1%; Score 25; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHWDGNEIDTQNRIDRM 62
Db 155 GNLRHWDGNEIDTQNRIDRM 179

RESULT 9
A44823
synaptosomal-associated protein SNAP-25 peptide 10B - rabbit (fragment)
N:Alternate names: superprotein peptide 10B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C:Accession: A44823
R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A:Reference number: A44823; MUID:92044785; PMID:1941090
A:Accession: A44823
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <LOE>
A:Experimental source: visual tissue
A>Note: sequence extracted from NCBI backbone (NCBIP.64256)
C:Keywords: membrane trafficking

Query Match 17.4%; Score 15; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.2e-09; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDEREQMAISGGFIR 15
Db 2 VDEREQMAISGGFIR 16

RESULT 10
S32362
SNAP receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S32362
R:Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Temp
Nature 362, 318-324, 1993
A:Title: SNAP receptors implicated in vesicle targeting and fusion.
A:Reference number: S32360; MUID:93205116; PMID:8455717
A:Accession: S32362
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <SOE>

Query Match 17.4%; Score 15; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.1e-09; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 HMAIDMGNEIDTQNR 56
Db 32 HMAIDMGNEIDTQNR 46

RESULT 11
S36812
probable synapse-associated 28K protein - bovine (fragments)

A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50481
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RIS>
A:Cross-references: GB:L22976; NID:G349430; PIDN:AAA16538.1; PID:G349431
C:Genetics:
A:Gene: SNAP-25

Query Match 29.1%; Score 25; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 7e-19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHWDGNEIDTQNRIDRM 62
Db 155 GNLRHWDGNEIDTQNRIDRM 179

RESULT 9
A44823
synaptosomal-associated protein SNAP-25 peptide 10B - rabbit (fragment)
N:Alternate names: superprotein peptide 10B
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C:Accession: A44823
R:Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A:Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A:Reference number: A44823; MUID:92044785; PMID:1941090
A:Accession: A44823
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <LOE>
A:Experimental source: visual tissue
A>Note: sequence extracted from NCBI backbone (NCBIP.64256)
C:Keywords: membrane trafficking

Query Match 17.4%; Score 15; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.2e-09; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDEREQMAISGGFIR 15
Db 2 VDEREQMAISGGFIR 16

RESULT 10
S32362
SNAP receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-May-1999
C:Accession: S32362
R:Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Temp
Nature 362, 318-324, 1993
A:Title: SNAP receptors implicated in vesicle targeting and fusion.
A:Reference number: S32360; MUID:93205116; PMID:8455717
A:Accession: S32362
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-46 <SOE>

Query Match 17.4%; Score 15; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 8.1e-09; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 HMAIDMGNEIDTQNR 56
Db 32 HMAIDMGNEIDTQNR 46

RESULT 11
S36812
probable synapse-associated 28K protein - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C:Accession: S36812
R:Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A:Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A:Reference number: S36811; MUID:93374072; PMID:8365494
A:Accession: S36812
A:Molecule type: protein
A:Residues: 1-56 <HOR>
A:Experimental source: brain

Query Match 14.0%; Score 12; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AISGGFIRRVTN 19
Db 35 AISGGFIRRVTN 46

RESULT 12
A49708
synaptosomal-associated 25K protein - rat (fragments)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 12-Jun-1998
C:Accession: A49708
R:Binz, I.; Blasi, J.; Yanasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.;
J. Biol. Chem. 269, 1617-1620, 1994
A:Title: Proteolysis of SNAP-25 by types E and A botulin neurotoxins.
A:Reference number: A49708; MUID:94124495; PMID:8294407
A:Accession: A49708
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-29 <BIN>

Query Match 12.8%; Score 11; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e-05; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 IMEKADSNKTR 71
Db 11 IMEKADSNKTR 21

RESULT 13
I50552
synapse protein - marbled electric ray
C:Species: Torpedo marmorata (marbled electric ray)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50552
R:Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertson, A.; Nassel, D.; Pieribone, V.
J. Biol. Chem. 269, 24408-24414, 1993
A:Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) si
A:Reference number: A49513; MUID:94043281; PMID:8226991
A:Accession: I50552
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-210 <RIS>
A:Cross-references: GB:L22020; NID:G431296; PIDN:AAA49284.1; PID:G431297

Query Match 11.6%; Score 10; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 0.0064; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHWDGNEIDTQNR 47
Db 165 GNLRHWDGNEIDTQNR 174

RESULT 14
JC5512
SNARE protein 23 - mouse

C:Species: Mus musculus (house mouse)
 C>Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
 C:Accession: J05512
 R:Araki, S.; Tamori, Y.; Kawanishi, M.; Shinoda, H.; Masugi, J.; Mori, H.; Niki, T.; Oka
 Biochem. Biophys. Res. Commun. 234, 257-262, 1997
 A:Title: Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c.
 A:Reference number: J05512; MUID:97312558; PMID:9168999
 A:Accession: J05512
 A:Molecule type: mRNA
 A:Residues: 1-210 <ARA>
 A:Cross-references: DBJ:AB000822; NID:g2189950; PIDN:BAA20345.1; PID:d1021177; PID:g218
 C:Comment: This protein is involved in the insulin-induced translocation of vesicles con

Query Match 11.6%; Score 10; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 0.0064;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 MALDMGNEID 52
 DB 168 MALDMGNEID 177

RESULT 15
 H89819
 conserved hypothetical protein SA0485 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: H89819
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: H89819
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-357 <KUR>
 A:Cross-references: GB:BA000018; PID:g13700417; PIDN:BAB41715.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA0485
 C:Superfamily: conserved hypothetical protein yacL

Query Match 9.3%; Score 8; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 FIRRVTNA 20
 DB 60 FIRRVTNA 67

RESULT 16
 H64529
 hypothetical protein HP0080 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
 C:Accession: H64529
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: H64529
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-593 <TOM>
 A:Cross-references: GB:AE000529; GB:AE000511; NID:g2313152; PIDN:AND07151.1; PID:g231316

Query Match 9.3%; Score 8; DB 2; Length 593;

Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNLR 41
 DB 81 SGILGNLR 88

RESULT 17
 A97278
 mannose-1-phosphate guanylyltransferase [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: A97278
 R:Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A97278
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-350 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK81012.1; PID:g15026135; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC3072

Query Match 8.1%; Score 7; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IMEXADS 67
 DB 254 IMEXADS 260

RESULT 18
 AH3144
 conserved hypothetical protein Atu4780 [imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AH3144
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH3144
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-362 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAL45574.1; PID:g17743290; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4780
 A:Map position: linear chromosome

Query Match 8.1%; Score 7; DB 2; Length 362;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 SGILGNL 40
 DB 227 SGILGNL 233

RESULT 19
 E30797
 hypothetical protein EC3149 [imported] - Escherichia coli (strain 0157:H7, substrain R.

C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Nov-2003
 C:Accession: E90797
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: E90797
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA034772.1; PID:gl3360809; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RMD 050952
 C:Genetics:
 A:Gene: ECa1349
 C:Superfamily: uncharacterized conserved protein

Query Match 8.1%; Score 7; DB 2; Length 380;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 RRVTHAR 21
 Db 150 RRVTHAR 156
 |||||

RESULT 20
 G95657
 hypothetical protein Z1608 [imported] - Escherichia coli (strain O157:H7, substrain EDL957)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Nov-2003
 C:Accession: G85606; F85606
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: G85657
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <STO>
 A:Cross-references: GB:AB005174; NID:gi2514491; PIDN:AG055723.1; GSPDB:GN00145; UWGP:Z16
 A:Experimental source: strain O157:H7, substrain EDL933
 A:Accession: F85606
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-380 <ST2>
 A:Cross-references: GB:AB005174; NID:gi2513974; PIDN:AG055314.1; GSPDB:GN00145; UWGP:Z11
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z1608; Z1169
 C:Superfamily: uncharacterized conserved protein

Query Match 8.1%; Score 7; DB 2; Length 380;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 15 RRVTHAR 21
 Db 150 RRVTHAR 156
 |||||

RESULT 21
 T19354
 hypothetical protein C17E4.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19354
 R:Percy, C.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19113
 A:Accession: T19354

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-386 <WIL>
 A:Cross-references: EMBL:Z81037; PIDN:CAB02748.1; GSPDB:GN00019; CESP:C17E4.10
 A:Experimental source: clone C17E4
 C:Genetics:
 A:Gene: CESP:C17E4.10
 A:Map position: 1
 A:Introns: 36/3; 98/2; 264/3; 309/2

Query Match 8.1%; Score 7; DB 2; Length 386;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 ENEEMDE 28
 Db 248 ENEEMDE 254
 |||||

RESULT 22
 C86640
 multidrug efflux transporter blt [imported] - Lactococcus lactis subsp. lactis (strain I
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: C86640
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: C86640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-387 <STO>
 A:Cross-references: GB:AE005176; PID:gi2722970; PIDN:AAK04221.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: blt

Query Match 8.1%; Score 7; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 AISGGFI 14
 Db 138 AISGGFI 144
 |||||

RESULT 23
 C98143
 hypothetical protein AGR_L206 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
 C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: C98143
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: C98143
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-396 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK88669.1; PID:gi5158398; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L206
 A:Map position: linear chromosome

Query Match 8.1%; Score 7; DB 2; Length 396;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 34 SGILGNL 40
 |||||


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Db      261  SGLGNL 267

RESULT 24
T45813
hypothetical protein F2809.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 23-Mar-2001
A:Accession: T45813
R:Benes, V.; Rechmann, S.; Borkova, D.; Ansoorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23014
A:Accession: T45813
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-875 <BEN>
A:Cross-references: EMBL:AL137080
A:Experimental source: cultivar Columbia; BAC clone F2809
C:Genetics:
A:Map position: 3
A:Introns: 48/2; 78/2; 100/3; 120/3; 150/3; 236/3; 313/3; 331/3; 359/3; 378/3; 67
A>Note: F2809.200
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g41620

Query Match      8.1%; Score 7; DB 2; Length 875;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      56  RQIDRIM 62
      |||||
Db      432  RQIDRIM 438

RESULT 25
T05647
hypothetical protein F20D10.320 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
A:Accession: T05647
R:Bevan, M.; Wedler, H.; Kutzner, M.; Vambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05647
A:Molecule type: DNA
A:Residues: 1-1643 <BEV>
A:Cross-references: EMBL:AL035538
A:Experimental source: cultivar Columbia; BAC clone F20D10
C:Genetics:
A:Map position: 4
A:Introns: 328/3; 444/2; 555/3; 696/3; 734/1; 819/3; 830/3; 994/2; 1101/3; 1222/1; 1442/
A>Note: F20D10.320

Query Match      8.1%; Score 7; DB 2; Length 1643;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      58  IDRIMEK 64
      |||||
Db      649  IDRIMEK 655

RESULT 26
T06119
hypothetical protein F23E12.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
A:Accession: T06119
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hobeisel,
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15485
A:Accession: T06119
A:Molecule type: DNA
A:Residues: 1-1711 <BEV>

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A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.60
A:Experimental source: cultivar Columbia; BAC clone F23E12
C:Genetics:
A:Gene: ATSP:F23E12.60
A:Map position: 4
A:Introns: 454/2; 572/3; 713/3; 811/2; 902/3; 1068/2; 1175/3; 1294/1; 1512/3

Query Match      8.1%; Score 7; DB 2; Length 1711;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      58  IDRIMEK 64
      |||||
Db      666  IDRIMEK 672

RESULT 27
E86151
hypothetical protein F22M8.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
A:Accession: E86151
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86151
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1750 <STO>
A:Cross-references: GB:AE005172; NID:g8570447; PIDN:AAF76474.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match      8.1%; Score 7; DB 2; Length 1750;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      58  IDRIMEK 64
      |||||
Db      707  IDRIMEK 713

RESULT 28
T47897
guanine nucleotide exchange factor-like protein - Arabidopsis thaliana
A:Alternate names: protein T4C21.270
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
A:Accession: T47897
R:Choisne, N.; Robert, C.; Bröttier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; S.
W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A:Reference number: Z24479
A:Accession: T47897
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1793 <CHO>
A:Cross-references: EMBL:AL162295
A:Experimental source: cultivar Columbia; BAC clone T4C21
C:Genetics:
A:Map position: 3
A:Introns: 401/2; 507/2; 622/3; 763/3; 861/2; 952/3; 1119/2; 1226/3; 1353/1; 1585/3
A>Note: T4C21.270

Query Match      8.1%; Score 7; DB 2; Length 1793;

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Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 IDRIMEK 64
|||||
Db 716 IDRIMEK 722

RESULT 29
T42409
FMRamide-like peptide 2b - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T42409
R;Li, C.; Nelson, L.S.; Memmott, J.M.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z22162
A:Accession: T42409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-75 <LIC>
A:Cross-references: EMBL:AF042388; PIDN:AAC08939.1
C:Genetics:
A:Gene: flp-2b

Query Match 7.0%; Score 6; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
|||||
Db 2 QVSGIL 7

RESULT 30
AH3402
hypothetical cytosolic protein BMEI1206 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AH3402
R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AH3402
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-84 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL52387.1; PID:gl7983187; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1206
A:Map position: 1

Query Match 7.0%; Score 6; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 LDMGNE 50
|||||
Db 41 LDMGNE 46

RESULT 31
T26263
FMRamide-like peptide 2a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T26263; T42408
R;Mortimore, B.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z20185

A:Accession: T26263
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-106 <WIL>
A:Cross-references: EMBL:Z49869; PIDN:CAA90031.1; GSPDB:GN00028; CESP:W07E11.3
A:Experimental source: clone W07E11
R;Li, C.; Nelson, L.S.; Memmott, J.M.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z22162
A:Accession: T42408
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-106 <LIC>
A:Cross-references: EMBL:AF042387; PIDN:AAC08938.1
C:Genetics:
A:Gene: flp-2a; W07E11.3a
A:Map position: X
A:Introns: 92/2

Query Match 7.0%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 QVSGIL 37
|||||
Db 2 QVSGIL 7

RESULT 32
T40946
60S ribosomal protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T40946
R;Lucas, M.; Gaillardin, C.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, January 1999
A:Reference number: Z21959
A:Accession: T40946
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-111 <LUC>
A:Cross-references: EMBL:AL035259; PIDN:CAA22868.1; GSPDB:GN00068; SPDB:SPCC1322.15
A:Experimental source: strain 972h-; cosmid cl322
C:Genetics:
A:Gene: SPDB:SPCC1322.15
A:Map position: 3
C:Superfamily: rat ribosomal protein L34

Query Match 7.0%; Score 6; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRI 72
|||||
Db 17 SNKTRI 22

RESULT 33
T17380
vrlA protein - Dichelobacter nodosus
C:Species: Dichelobacter nodosus
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17380
R;Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, A.
Infect. Immun. 67, 1277-1286, 1999
A:Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) of
A:Reference number: Z18734; MUID:99150261; PMID:10024571
A:Accession: T17380
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-118 <BIL>
A:Cross-references: EMBL:U20246; NID:g3493323; PID:g3482862; PIDN:AAC33389.1
A:Experimental source: strain A198

Query Match 7.0%; Score 6; DB 2; Length 118;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
 |||||
 Db 80 LEQVSG 85

RESULT 34
 D82022
 truncated pilin NMA0272 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
 C:Species: Neisseria meningitidis
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
 C:Accession: D82022
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 ; Holroyd, S.; Jagels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: D82022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-120 <PAR>
 A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83580.1; PID:g737903
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: pilS8; NMA0272

Query Match 7.0%; Score 6; DB 2; Length 120;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 GNEIDT 53
 |||||
 Db 49 GNEIDT 54

RESULT 35
 E89984
 hypothetical protein SA1762 [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: E89984
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89759; MUID:21311952; PMID:11418146
 A:Accession: E89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-124 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701745; PIDN:BAB43038.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA1762

Query Match 7.0%; Score 6; DB 2; Length 124;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 DENLEQ 32
 |||||
 Db 62 DENLEQ 67

RESULT 36
 AH3491
 hypothetical cytosolic protein BME11918 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AH3491
 R:DelVecchio, V.G.; Kaparal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AH3491
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-127 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAL53099.1; PID:g17983964; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BME11918
 A:Map position: 1

Query Match 7.0%; Score 6; DB 2; Length 127;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 VSGILG 38
 |||||
 Db 112 VSGILG 117

RESULT 37
 T46908
 hypothetical protein DKFp761G2423.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 19-May-2000
 C:Accession: T46908
 R:Blöcker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Weill, B.; Wiemann, S.
 submitted to the Protein Sequence Database, February 2000
 A:Reference number: Z24137
 A:Accession: T46908
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-138 <AAA>
 A:Cross-references: EMBL:AL136571
 A:Experimental source: adult amygdala, clone DKFp761G2423
 C:Genetics:
 A:Note: DKFp761G2423.1
 C:Superfamily: Saccharomyces probable membrane protein YMR292w

Query Match 7.0%; Score 6; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFIRRV 17
 |||||
 Db 107 GFIRRV 112

RESULT 38
 T39245
 ef-hand protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
 C:Accession: T39245
 R:Wiedler, H.; Duesterhoeft, A.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z21742
 A:Accession: T39245
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-141 <WED>
 A:Cross-references: EMBL:AL117210; PIDN:CAB55175.1; GSPDB:GN00066; SPDB:SPAP8A3.08
 A:Experimental source: strain 972h-; clone p1 p8A3
 C:Genetics:
 A:Gene: SPDB:SPAP8A3.08
 A:Map position: 1
 A:Introns: 11/1; 55/1; 102/1; 133/1

C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand

Query Match 7.0%; Score 6; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 NEEUDE 28
|||||
DB 112 NEEUDE 117

RESULT 39

C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
C:Accession: C44259

R:Aizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.

J. Cell Biol. 119, 1287-1296, 1992

A:Title: Kinesin family in murine central nervous system.

A:Reference number: A44259; MUID:93077686; PMID:1447303

A:Accession: C44259

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-143 <AIZ>

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIP:118906)

C:Superfamily: kinesin heavy chain; kinesin motor domain homology

F:1-143/Domain: kinesin motor domain homology (fragment) <XMOT>

Query Match

Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 MDENLE 31
|||||
DB 35 MDENLE 40

RESULT 40

S31243
ribosomal protein Yml28 precursor, mitochondrial - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YDR462W

C:Species: Saccharomyces cerevisiae

C:Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 19-Apr-2002

C:Accession: S31243; S69630; S17269

R:Wang, S.S.; Stanford, D.R.; Silvers, C.D.; Hopper, A.K.

Mol. Cell. Biol. 12, 2633-2643, 1992

A:Title: STP1, a gene involved in pre-rRNA processing, encodes a nuclear protein contain

A:Reference number: S31243; MUID:92269836; PMID:1588961

A:Accession: S31243

A:Molecule type: DNA

A:Residues: 1-147 <WAN>

A:Cross-references: EMBL:M88597; NID:g172767; PIDN:AAA35123.1; PID:g172768

R:DiTreich, F.S.

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.

A:Reference number: S69534

A:Accession: S69630

A:Molecule type: DNA

A:Residues: 1-147 <DIE>

A:Cross-references: EMBL:U33050; NID:g927726; PID:g927728; MIPS:YDR462W

R:Grohmann, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.

FEBS Lett. 284, 51-56, 1991

A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from

A:Reference number: S17255; MUID:91285106; PMID:2060626

A:Accession: S17269

A:Molecule type: protein

A:Residues: 'KIF', 30-32, 'VI', 35, 'VI', 38-43, 'X', 45-46, 'X', 48, 'KX', 51-52, 'P' <GRO>

A:Experimental source: strain 07173

C:Genetics:

A:Gene: SGD:MRPL28; MRPL28

A:Cross-references: MIPS:YDR462W; SGD:S0002870

A:Map position: 4R

A:Genome: nuclear

C:Keywords: mitochondrion; protein biosynthesis; ribosome

F:1-26/Domain: transit peptide (mitochondrion) #status experimental <TNP>

F:27-147/Product: ribosomal protein Yml28 #status experimental <MAT>

Query Match 7.0%; Score 6; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 LEQVSG 35
|||||

DB 14 LEQVSG 19

RESULT 41

G95210

acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: G95210

R:Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hei

on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

son, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: G95210

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75880.1; PID:g14973306; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1807

Query Match

Best Local Similarity 100.0%; Pred. No. 84;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EANQRA 79
|||||

DB 115 EANQRA 120

RESULT 42

A98075

conserved hypothetical protein spr1627 [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C:Accession: A98075

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; I

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; I

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: A98075

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <KUR>

A:Cross-references: GB:AE007317; PIDN:AAL00430.1; PID:g15459287; GSPDB:GN00174

C:Genetics:

A:Gene: spr1627

Query Match

Best Local Similarity 100.0%; Pred. No. 84;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 EANQRA 79

```

Db      115 EANDRA 120
|||||
RESULT 43
AC1608
arginine repressor homolog lin1404 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AC1608
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1608
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <GLA>
A:Cross-references: GB:AL592022; PIDN:CA96635.1; PID:gi16413877; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1404
C:Superfamily: Escherichia coli arginine repressor argR

Query Match      7.0%; Score 6; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      49 NEIDTQ 54
|||||
Db      17 NEIDTQ 22

RESULT 44
AG1245
arginine repressor homolog lmo1367 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AG1245
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1245
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CA99445.1; PID:gi16410783; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1367
C:Superfamily: Escherichia coli arginine repressor argR

Query Match      7.0%; Score 6; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      49 NEIDTQ 54
|||||
Db      17 NEIDTQ 22

RESULT 45
AB3053
conserved hypothetical protein PA4746 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: AB3053
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: AB3053
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <STO>
A:Cross-references: GB:AE004888; GB:AE004091; NID:99951001; PIDN:AG08132.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4746
C:Superfamily: nus operon 15K protein

Query Match      7.0%; Score 6; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      32 QVSGIL 37
|||||
Db      58 QVSGIL 63

Search completed: March 4, 2004, 08:34:44
Job time : 22 secs

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Query Match 57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 158 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206
RESULT 8
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Staifford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; ORGANISM: Mus musculus

Query Match 57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 158 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206
RESULT 8
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Staifford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; ORGANISM: Mus musculus

Fri Mar 5 07:11:12 2004

us-10-030-485a-4.rapb

Page 1

OM protein - protein search, using sw model
Run on: March 4, 2004, 08:32:56 ; Search time 34 Seconds
(without alignments)
534.094 Million cell updates/sec
Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGGFIRRTNA.....SNKTRIDEANORATKMLGSG 86
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 809742 seqs, 211153259 residues
Word size : 0
Total number of hits satisfying chosen parameters: 809742
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries
Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pap.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pap.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
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Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 158 GNLHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 206
RESULT 8
US-09-962-360B-12
; Sequence 12, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Staifford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; ORGANISM: Mus musculus

US-09-962-360B-11
; Sequence 11, Application US/09962360B
; Publication No. US20030077685A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt, James J.
; APPLICANT: Staifford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050

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Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 3
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7
Query Match 57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Fri Mar 5 07:11:12 2004

us-10-030-485a-4.rapb

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-33
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Best Local Similarity 100.0%; Pred. No. 8.3e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33
RESULT 12
US-09-942-098-38
; Sequence 38, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-38
Query Match 38.4%; Score 33; DB 10; Length 33;
Best Local Similarity 100.0%; Pred. No. 8.3e-27;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33

; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2
Query Match 57.0%; Score 49; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 6
US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2
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Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
DB 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 14
US-09-942-024-16

us-10-030-485a-4.rapb

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43057
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL023913.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.1
; OTHER INFORMATION: EST HUMAN HIT: AA663884.1, EVALUATE 9.00e-21
; OTHER INFORMATION: SWISSPROT HIT: P13795, EVALUATE 7.00e-22
US-09-864-761-43057
Query Match 31.4%; Score 27; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEK 64
DB 22 GNLRHMDMGNEIDTQNRQIDRIMEK 48
RESULT 14
US-09-942-024-16

```
RESULT 15
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16

Query Match 31.4%; Score 27; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDLMGNEIDTQNRQIDRIM 64
Db 158 GNLRHWDLMGNEIDTQNRQIDRIM 184

RESULT 16
US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-14

Query Match 29.1%; Score 25; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDLMGNEIDTQNRQIDRIM 62
Db 155 GNLRHWDLMGNEIDTQNRQIDRIM 179

RESULT 17
US-09-942-098-14
; Sequence 14, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
```

```
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-14

Query Match 29.1%; Score 25; DB 10; Length 203;
Best Local Similarity 100.0%; Pred. No. 7.7e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDLMGNEIDTQNRQIDRIM 62
Db 155 GNLRHWDLMGNEIDTQNRQIDRIM 179

RESULT 18
US-09-942-024-90
; Sequence 90, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-90

Query Match 25.6%; Score 22; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ADSNKRTRIDEANQRATKMLGSG 86
Db 2 ADSNKRTRIDEANQRATKMLGSG 23

RESULT 19
US-09-942-098-90
; Sequence 90, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
```



```

; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 24
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
; US-09-942-098-90

Query Match          25.6%; Score 22; DB 10; Length 24;
Best Local Similarity 100.0%; Pred.No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ADSNKTTRIDEANQRATKMLGSG 86
      |||||||
DB 2 ADSNKTTRIDEANQRATKMLGSG 23

RESULT 20
US-09-942-024-37
; Sequence 37, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Carassius auratus
; US-09-942-024-37

Query Match          25.6%; Score 22; DB 10; Length 33;
Best Local Similarity 100.0%; Pred.No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 ADSNKTTRIDEANQRATKMLGSG 86
      |||||||
DB 12 ADSNKTTRIDEANQRATKMLGSG 33

RESULT 21
US-09-942-098-37
; Sequence 37, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0

```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 23
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-88

```

```

Query Match      24.4%; Score 21; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 66 DSNKTRIDEANQRATKMLGSG 86
Db 2 DSNKTRIDEANQRATKMLGSG 22

```

```

RESULT 24
US-09-942-024-89
; Sequence 89, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-89

```

```

Query Match      22.1%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 65 ADSNKTIDEANQRATKML 83
Db 2 ADSNKTIDEANQRATKML 20

```

```

RESULT 25
US-09-942-098-89
; Sequence 89, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

```

```

; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 21
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-89

```

```

Query Match      22.1%; Score 19; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 65 ADSNKTIDEANQRATKML 83
Db 2 ADSNKTIDEANQRATKML 20

```

```

RESULT 26
US-09-942-024-32
; Sequence 32, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: at the C-terminal
US-09-942-024-32

```

```

Query Match      20.9%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 66 DSNKTRIDEANQRATKML 83
Db 1 DSNKTRIDEANQRATKML 18

```

```

RESULT 27
US-09-942-098-32
; Sequence 32, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins

```

; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-32

Query Match 20.9%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANQRATKML 83
| | | | | | | | | | | | | | | | | |
Db 1 DSNKTRIDEANQRATKML 18

RESULT 28
US-09-942-024-93
; Sequence 93, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-93

Query Match 20.9%; Score 18; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 KTRIDEANQRATKMLGSG 86
| | | | | | | | | | | | | | | | | |
Db 4 KTRIDEANQRATKMLGSG 21

RESULT 29
US-09-942-098-93
; Sequence 93, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098

; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa-fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 22
; OTHER INFORMATION: Xaa-tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-93

Query Match 20.9%; Score 18; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 KTRIDEANQRATKMLGSG 86
| | | | | | | | | | | | | | | | | |
Db 4 KTRIDEANQRATKMLGSG 21

RESULT 30
US-09-942-024-30
; Sequence 30, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-30

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATKML 83
| | | | | | | | | | | | | | | | | |
Db 1 SNKTRIDEANQRATKML 17

RESULT 31
US-09-942-024-31
; Sequence 31, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-31

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANORATKM 82
Db 1 DSNKTRIDEANORATKM 17
|||||

RESULT 32
US-09-942-098-30
; Sequence 30, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-30

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANORATKM 83
Db 1 SNKTRIDEANORATKM 17
|||||

RESULT 33
US-09-942-098-31
; Sequence 31, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-31

Query Match 19.8%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 DSNKTRIDEANORATKM 82
|||||

Db 1 DSNKTRIDEANORATKM 17

RESULT 34
US-10-011-588-2
; Sequence 2, Application US/10011588
; Publication No. US20020168727A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Leonard
; APPLICANT: Jensen, Melody
; TITLE OF INVENTION: RECOMBINANT LIGHT CHAINS OF BOTULINUM
; TITLE OF INVENTION: NEUROTOXINS AND LIGHT CHAIN FUSION PROTEINS FOR USE IN
; TITLE OF INVENTION: RESEARCH AND CLINICAL THERAPY
; FILE REFERENCE: A34796 067252.0113
; CURRENT APPLICATION NUMBER: US/10/011,588
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 09/910,186
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/246,744
; PRIOR FILING DATE: 2000-11-06
; PRIOR APPLICATION NUMBER: 60/311,966
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: Residues 187-203 of SNAP-25
US-10-011-588-2

Query Match 19.8%; Score 17; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANORATKM 83
Db 1 SNKTRIDEANORATKM 17
|||||

RESULT 35
US-09-942-024-92
; Sequence 92, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION

```
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-92

Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORATKMLGSG 86
   |||||
Db 2 TRIDEANORATKMLGSG 18

RESULT 36
US-09-942-024-95
; Sequence 95, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Serotype Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=EDANS modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-95

Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORATKMLGSG 86
   |||||
Db 2 TRIDEANORATKMLGSG 18

RESULT 37
US-09-942-024-95
; Sequence 92, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-95

Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORATKMLGSG 86
   |||||
Db 2 TRIDEANORATKMLGSG 18

RESULT 38
US-09-942-098-95
; Sequence 95, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 19
; OTHER INFORMATION: Xaa=DABCYL modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-95

Query Match      19.8%; Score 17; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORATKMLGSG 86
   |||||
Db 2 TRIDEANORATKMLGSG 18

RESULT 39
US-09-942-024-29
; Sequence 29, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
```

```
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-29

Query Match      18.6%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQRTKM 82
Db      1 SNKTRIDEANQRTKM 16

RESULT 40
US-09-942-098-29
; Sequence 29, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-29

Query Match      18.6%; Score 16; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      67 SNKTRIDEANQRTKM 82
Db      1 SNKTRIDEANQRTKM 16

RESULT 41
US-09-942-024-85
; Sequence 85, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-85

Query Match      18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 NKTRIDEANQRTKML 83
Db      3 NKTRIDEANQRTKML 18

RESULT 42
US-09-942-098-85
; Sequence 85, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-85

Query Match      18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 NKTRIDEANQRTKML 83
Db      3 NKTRIDEANQRTKML 18

RESULT 43
US-09-942-024-28
; Sequence 28, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
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```
; FILE REFERENCE: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-024-85

Query Match      18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 NKTRIDEANQRTKML 83
Db      3 NKTRIDEANQRTKML 18

RESULT 42
US-09-942-098-85
; Sequence 85, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=fluorescein-modified lysine
; NAME/KEY: MOD_RES
; LOCATION: 20_
; OTHER INFORMATION: Xaa=tetramethylrhodamine-modified lysine
; NAME/KEY: AMIDATION
; LOCATION: (0)...(0)
; OTHER INFORMATION: at the C-terminal
US-09-942-098-85

Query Match      18.6%; Score 16; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      68 NKTRIDEANQRTKML 83
Db      3 NKTRIDEANQRTKML 18

RESULT 43
US-09-942-024-28
; Sequence 28, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
; NAME/KEY: MOD_RES
; LOCATION: 1
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-28

Query Match 17.4%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANORATK 81
Db 1 SNKTRIDEANORATK 15

RESULT 44

US-09-942-098-28
; Sequence 28, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-28

Query Match 17.4%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANORATK 81
Db 1 SNKTRIDEANORATK 15

RESULT 45

US-09-942-024-44
; Sequence 44, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-942-024-44

Query Match 17.4%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANORATK 81
Db 1 SNKTRIDEANORATK 15

Search completed: March 4, 2004, 08:36:05
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:31:50 ; Search time 22 Seconds
(without alignments)
201.811 Million cell updates/sec

Title: US-10-030-485A-4
Perfect score: 86
Sequence: 1 VDREQMAISGGFIRRVINA.....SNKTRIDANQATKMLGSG 86

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp:*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp:*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp:*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp:*
- 5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pcp:*
- 6: /cgn2_6/ptodata/2/iaa/backfile1.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	57.0	70	2	US-08-760-001-10
2	49	57.0	70	3	US-09-015-960-10
3	49	57.0	70	4	US-09-534-572-10
4	49	57.0	206	1	US-08-393-985-18
5	49	57.0	206	3	US-08-819-286-1
6	37	43.0	37	3	US-08-819-286-4
7	26	30.2	26	3	US-08-819-286-8
8	20	23.3	20	3	US-08-819-286-7
9	20	23.3	20	3	US-08-819-286-9
10	17	19.8	17	2	US-08-743-894B-1
11	17	19.8	17	2	US-08-743-894B-37
12	16	18.6	16	2	US-08-743-894B-49
13	16	18.6	16	3	US-08-819-286-12
14	15	17.4	15	2	US-08-743-894B-25
15	15	17.4	15	2	US-08-743-894B-38
16	15	17.4	17	2	US-08-743-894B-24
17	14	16.3	17	2	US-08-743-894B-28
18	13	15.1	17	2	US-08-743-894B-31
19	13	15.1	13	4	US-09-976-535A-1
20	13	15.1	17	2	US-08-743-894B-19
21	13	15.1	17	2	US-08-743-894B-25
22	13	15.1	17	2	US-08-743-894B-32
23	12	14.0	12	3	US-08-743-894B-41
24	12	14.0	13	3	US-08-750-101-11
25	12	14.0	14	4	US-09-976-535A-2
26	12	14.0	17	2	US-08-743-894B-27
27	12	14.0	17	2	US-08-743-894B-36

28	12	14.0	17	2	US-08-743-894B-39	Sequence 39, Appl
29	12	14.0	17	2	US-08-743-894B-42	Sequence 42, Appl
30	11	12.8	13	2	US-08-743-894B-16	Sequence 16, Appl
31	11	12.8	13	4	US-09-976-535A-13	Sequence 13, Appl
32	11	12.8	16	2	US-08-743-894B-51	Sequence 51, Appl
33	11	12.8	16	2	US-08-743-894B-52	Sequence 52, Appl
34	11	12.8	16	2	US-08-743-894B-54	Sequence 54, Appl
35	11	12.8	17	2	US-08-743-894B-2	Sequence 2, Appl
36	11	12.8	17	2	US-08-743-894B-6	Sequence 6, Appl
37	11	12.8	17	2	US-08-743-894B-43	Sequence 43, Appl
38	11	12.8	17	2	US-08-743-894B-44	Sequence 44, Appl
39	11	12.8	17	2	US-08-743-894B-45	Sequence 45, Appl
40	11	12.8	17	2	US-08-743-894B-47	Sequence 47, Appl
41	10	11.6	12	2	US-08-743-894B-17	Sequence 17, Appl
42	10	11.6	13	4	US-09-976-535A-11	Sequence 11, Appl
43	10	11.6	13	4	US-09-976-535A-12	Sequence 12, Appl
44	10	11.6	14	4	US-09-976-535A-6	Sequence 6, Appl
45	10	11.6	16	2	US-08-743-894B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-760-001-10
; Sequence 10, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. P.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-760-001-10

Query Match 57.0%; Score 49; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 22 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 70

RESULT 2

US-09-015-960-10
; Sequence 10, Application US/09015960
; Patent No. 6043042
; GENERAL INFORMATION:
; APPLICANT: Stone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Emond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-015-960-10

Query Match 57.0%; Score 49; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 22 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 70

RESULT 3

US-09-534-572-10
; Sequence 10, Application US/09534572
; Patent No. 6337386
; GENERAL INFORMATION:
; APPLICANT: Stone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/534,572
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/015,960
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,001
; FILING DATE: 30-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Emond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-534-572-10

Query Match 57.0%; Score 49; DB 4; Length 70;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 86
Db 22 GNLRHWDGNEIDTQNRQIDRIMEKADSNKTRIDEANORATKMLGSG 70

RESULT 4

US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0152
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-393-985-18

Query Match 57.0%; Score 49; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 5
US-08-819-286-1
Sequence 1, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 206 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 57.0%; Score 49; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86

Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
RESULT 6
US-08-819-286-4
Sequence 4, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-4

Query Match 43.0%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 50 EIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 1 EIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 37

RESULT 7
US-08-819-286-8
Sequence 8, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-8

Query Match 30.2%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 IMEKADSNKTRIDEANQATKMLGSG 86
Db 1 IMEKADSNKTRIDEANQATKMLGSG 26

RESULT 8
US-08-819-286-7
Sequence 7, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-7
Query Match 23.3%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 EIDTQNRQIDRIMEKADSNK 69
Db 1 EIDTQNRQIDRIMEKADSNK 20
RESULT 9
US-08-819-286-9
Sequence 9, Application US/08819286
Patent No. 6169074
GENERAL INFORMATION:
APPLICANT: Montal, Mauricio
TITLE OF INVENTION: PEPTIDE INHIBITORS OF
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,286
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,599
FILING DATE: 18-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Taylor, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07349/005001
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-819-286-9

Query Match 23.3%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 SNKTRIDEANQATKMLGSG 86
Db 1 SNKTRIDEANQATKMLGSG 20

RESULT 10
US-08-743-894B-1
Sequence 1, Application US/08743894B

Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-743-894B-1

Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANORATKML 83
Db 1 SNKTRIDEANORATKML 17

RESULT 11
US-08-743-894B-37
Sequence 37, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-49

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-37

Query Match 19.8%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANORATKML 83
Db 1 SNKTRIDEANORATKML 17

RESULT 12
US-08-743-894B-49
Sequence 49, Application US/08743894B
Patent No. 5965699
GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-49

Query Match 18.6%; Score 16; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRAATK 82
Db 1 SNKTRIDEANQRAATK 16

RESULT 13
US-08-819-286-12
; Sequence 12, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-12

Query Match 18.6%; Score 16; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 QNRQIDRIMEKADSNK 69
Db 1 QNRQIDRIMEKADSNK 16

RESULT 14
US-08-743-894B-38
; Sequence 38, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty

STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-38

Query Match 17.4%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRAATK 81
Db 1 SNKTRIDEANQRAATK 15

RESULT 15
US-08-743-894B-24
; Sequence 24, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
LOCATION: 16
OTHER INFORMATION: Xaa represents norleucine
US-08-743-894B-24

Query Match 17.4%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATK 81
Db 1 SNKTRIDEANQRATK 15

RESULT 16
US-08-743-894B-28
; Sequence 28, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILLING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; OTHER INFORMATION: Xaa represents norleucine
US-08-743-894B-28

Query Match 17.4%; Score 15; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.3e-09;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRATK 81

Db 1 SNKTRIDEANQRATK 15

RESULT 17
US-08-743-894B-31
; Sequence 31, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILLING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; OTHER INFORMATION: Xaa represents norleucine
US-08-743-894B-31

Query Match 16.3%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.8e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRAT 80
Db 1 SNKTRIDEANQRAT 14

RESULT 18
US-09-976-535A-1
; Sequence 1, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Baton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: human
; US-09-976-535A-1

Query Match          15.1%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORATKML 82
Db 1 TRIDEANORATKML 13

RESULT 19
US-08-743-894B-19
; Sequence 19, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
; US-08-743-894B-19

Query Match          15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQRA 79
Db 1 SNKTRIDEANQRA 13

RESULT 21
US-08-743-894B-26
; Sequence 26, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represents Abu, or 2-Aminobutyric Acid
; US-08-743-894B-19

Query Match          15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANQRAATKML 83
Db 5 RIDEANQRAATKML 17

RESULT 20
US-08-743-894B-25
; Sequence 25, Application US/08743894B
; Patent No. 5965699
```

APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
US-08-743-894B-26

Query Match 15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 67 SNKTRIDEANORA 79
Db 1 SNKTRIDEANORA 13

RESULT 22

US-08-743-894B-32
Sequence 32, Application US/08/743894B
Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:

US-08-743-894B-32

Query Match 15.1%; Score 13; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 67 SNKTRIDEANORA 79
Db 1 SNKTRIDEANORA 13

RESULT 23

US-08-743-894B-41
Sequence 41, Application US/08/743894B
Patent No. 5965699

GENERAL INFORMATION:
APPLICANT: James J. Schmidt
APPLICANT: Karen A. Bostian
TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
STREET: USA MCMC - 504 Scott Street
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,894B
FILING DATE: No. 5965699ember 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid sequence
STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:

US-08-743-894B-41

Query Match 14.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 72 IDEANORATKML 83
Db 1 IDEANORATKML 12

RESULT 24

US-08-750-101-11
Sequence 11, Application US/08/750101B
Patent No. 6203794

GENERAL INFORMATION:
APPLICANT: Dolly, James Oliver
APPLICANT: Aoki, Roger Kei
APPLICANT: Wheeler, Larry
APPLICANT: Elwood, Micheal


```
; TITLE OF INVENTION: MODIFICATION OF CLOSTRIDIAL TOXINS FOR
; TITLE OF INVENTION: USE AS TRANSPORT PROTEINS
; FILE REFERENCE: 17044
; CURRENT APPLICATION NUMBER: US/08/750,101B
; EARLIER FILING DATE: 1997-05-01
; EARLIER APPLICATION NUMBER: PCT/GB/01253
; EARLIER FILING DATE: 1995-05-31
; EARLIER APPLICATION NUMBER: UK 9410871.9
; EARLIER FILING DATE: 1994-05-31
; EARLIER APPLICATION NUMBER: UK 9410871.1
; EARLIER FILING DATE: 1994-05-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Portion of predicted amino acid sequence of human
; OTHER INFORMATION: SNAP-25.
US-08-750-101-11

Query Match 14.0%; Score 12; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ANQATKMLGSG 86
Db 2 ANQATKMLGSG 13

RESULT 25
US-09-976-535A-2
; Sequence 2, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
; NAME/KEY: misc feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa represents D-Lys
US-09-976-535A-2

Query Match 14.0%; Score 12; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQATK 81
Db 1 TRIDEANQATK 12

RESULT 26
US-08-743-894B-27
; Sequence 27, Application US/08743894B
; Patent No. 5965699
```

```
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 27:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 13
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-27

Query Match 14.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SNKTRIDEANQR 78
Db 1 SNKTRIDEANQR 12

RESULT 27
US-08-743-894B-36
; Sequence 36, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
```

;	STATUS: Single
;	APPLICANT: ADREN A. BOSCHIAN
;	;
;	TOPIC: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
;	TOPOLOGY: Linear
;	FEATURE:
;	NUMBER OF SEQUENCES: 56

```

QY 72 IDEANQATKM 82
DB 3 IDEANQATKM 13

RESULT 32
US-08-743-894B-51
; Sequence 51, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMCM - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: NO. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-51
Query Match 12.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANQAT 80
DB 4 TRIDEANQAT 14

RESULT 33
US-08-743-894B-52
; Sequence 52, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MMCM - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND

```

```
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; LOCATION: 16
; OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
US-08-743-894B-52

Query Match 12.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
Db 4 TRIDEANORAT 14

RESULT 34
US-08-743-894B-54
; Sequence 54, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Postian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; LOCATION: 16
; OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
US-08-743-894B-54

Query Match 12.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
Db 4 TRIDEANORAT 14

RESULT 35
US-08-743-894B-2
; Sequence 2, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Postian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; LOCATION: 16
; OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
US-08-743-894B-2

Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
Db 4 TRIDEANORAT 14
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 16
; OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
US-08-743-894B-54

Query Match 12.8%; Score 11; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
Db 4 TRIDEANORAT 14

RESULT 35
US-08-743-894B-2
; Sequence 2, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Postian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; LOCATION: 16
; OTHER INFORMATION: Xaa represents Nle, or No. 5965699leucine
US-08-743-894B-2

Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 TRIDEANORAT 80
Db 4 TRIDEANORAT 14
```

RESULT 36
US-08-743-894B-6
; Sequence 6, Application US/08/743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743 894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 16
; OTHER INFORMATION: Xaa represent Nle, or No. 5965699leucine
US-08-743-894B-6
Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 70 TRIDEANQRAT 80
DB 4 TRIDEANQRAT 14
RESULT 37
US-08-743-894B-43
; Sequence 43, Application US/08/743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743 894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; US-08-743-894B-43
Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 67 SNKTRIDEANQ 77
DB 1 SNKTRIDEANQ 11
RESULT 38
US-08-743-894B-44
; Sequence 44, Application US/08/743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Atty
; STREET: USA MCMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743 894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; INFORMATION FOR SEQ ID NO: 44:
; US-08-743-894B-44

```

US-08-743-894B-47
; Sequence 47, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Att'y
; STREET: USA MMRC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-47
Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANOQ 77
Db 1 SNKTRIDEANOQ 11

RESULT 41
US-08-743-894B-17
; Sequence 17, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn:John Moran-Patent Att'y
; STREET: USA MMRC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
;
US-08-743-894B-45
Query Match 12.8%; Score 11; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SNKTRIDEANOQ 77
Db 1 SNKTRIDEANOQ 11

RESULT 40

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/743,894B
;; FILING DATE: No. 596569 September 6, 1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Charles H. Harris
;; REGISTRATION NUMBER: 34,616
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 619-2065
;; TELEFAX: (301) 619-7714
;; INFORMATION FOR SEQ ID NO: 17:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid sequence
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
;; FEATURE:
;; US-08-743-894B-17

Query Match 11.6%; Score 10; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 71 RIDEANORAT 80
|||||
DB 1 RIDEANORAT 10

RESULT 42

US-09-976-535A-11
; Sequence 11, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 13
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
US-09-976-535A-11

Query Match 11.6%; Score 10; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANORATK 81
|||||
DB 3 IDEANORATK 12

RESULT 43

US-09-976-535A-12
; Sequence 12, Application US/09976535A

;; Patent No. 6504006
;; GENERAL INFORMATION:
;; APPLICANT: Shine, Nancy R.
;; APPLICANT: Crawford, Karen R.
;; APPLICANT: Eaton, Linda J.
;; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
;; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
;; FILE REFERENCE: P010018
;; CURRENT APPLICATION NUMBER: US/09/976,535A
;; CURRENT FILING DATE: 2001-10-12
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12
;; LENGTH: 13
;; TYPE: PRT
;; ORGANISM: artificial sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide
;; NAME/KEY: misc feature
;; LOCATION: (2)..(2)
;; OTHER INFORMATION: Xaa represents D-Arg
;; NAME/KEY: misc feature
;; LOCATION: (13)..(13)
;; OTHER INFORMATION: Leu represents norleucine
US-09-976-535A-12

Query Match 11.6%; Score 10; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANORATK 81
|||||
DB 3 IDEANORATK 12

RESULT 44

US-09-976-535A-6
; Sequence 6, Application US/09976535A
; Patent No. 6504006
; GENERAL INFORMATION:
; APPLICANT: Shine, Nancy R.
; APPLICANT: Crawford, Karen R.
; APPLICANT: Eaton, Linda J.
; TITLE OF INVENTION: Substrate Peptides and Assays for Detecting and Measuring Proteol
; TITLE OF INVENTION: Activity of Serotype A Neurotoxin from Clostridium botulinum
; FILE REFERENCE: P010018
; CURRENT APPLICATION NUMBER: US/09/976,535A
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: Xaa represents D-Arg
; NAME/KEY: misc feature
; LOCATION: (13)..(13)
; OTHER INFORMATION: Leu represents norleucine
US-09-976-535A-6

Query Match 11.6%; Score 10; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 IDEANORATK 81
|||||
DB 3 IDEANORATK 12

RESULT 45
US-08-743-894B-7
; Sequence 7, Application US/08743894B
; Patent No. 5965699
; GENERAL INFORMATION:
; APPLICANT: James J. Schmidt
; APPLICANT: Karen A. Bostian
; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin fr
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MCMR-JA Attn: John Moran-Patent Atty
; STREET: USA MMC - 504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,894B
; FILING DATE: No. 5965699ember 6, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid sequence
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; FEATURE:
; LOCATION: 4
; OTHER INFORMATION: Xaa represent Abu, or 2-Aminobutyric Acid
US-08-743-894B-7

Query Match 11.6%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 71 RIDEANQRAT 80
| | | | | | | |
Db 5 RIDEANQRAT 14

Search completed: March 4, 2004, 08:35:18
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:27:55 ; Search time 54 Seconds
(without alignments)
449.983 Million cell updates/sec

Title: US-10-030-485A-4

Perfect score: 86
Sequence: 1 VDREQMAISGGFIRVTNA.....SNKTRIDEANQRATKMLGSG 86

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: A.GeneSeq_29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1908s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	86	4	AAB15584 Human SNA
2	49	57.0	70	2	AAR86823 SNAP-25 r
3	49	57.0	116	5	AAO15165 Clostridi
4	49	57.0	206	2	AAW30103 Synaptoso
5	49	57.0	206	2	AAW43426 Mouse syn
6	49	57.0	206	2	AAW79198 Mouse SNA
7	49	57.0	206	4	AAU00246 Synaptoso
8	49	57.0	206	4	AAU00253 SNARE hom
9	49	57.0	206	4	AAU00252 SNARE hom
10	49	57.0	206	6	AAE36662 Human SNA
11	49	57.0	206	6	AAE36667 Rat VAMP-
12	49	57.0	206	7	ADe54280 Rat Prote
13	49	57.0	206	7	ADe54288 Rat Prote
14	49	57.0	206	7	ADe54276 Rat Prote
15	49	57.0	206	7	ADe54290 Human Pro
16	49	57.0	206	7	ADe54282 Rat Prote
17	49	57.0	206	7	ADe54274 Rat Prote
18	49	57.0	206	7	ADe54286 Human Pro
19	49	57.0	206	7	ADe54284 Rat Prote
20	49	57.0	206	7	ADe54272 Rat Prote
21	49	57.0	206	7	ADe54278 Rat Prote
22	45	52.3	206	4	AAU02640 Synaptoso
23	44	51.2	206	4	AAU02638 Synaptoso
24	41	47.7	198	4	AAU00255 Synaptoso
25	40	46.5	116	5	AAO15166 Clostridi

26	40	46.5	199	4	AAU00263 Synaptoso
27	40	46.5	200	4	AAU00264 Synaptoso
28	40	46.5	201	4	AAU02637 Synaptoso
29	40	46.5	202	4	AAU00265 Synaptoso
30	40	46.5	203	4	AAU02636 Synaptoso
31	40	46.5	205	4	AAU00261 Synaptoso
32	40	46.5	206	4	AAU02171 Synaptoso
33	40	46.5	206	4	AAU00259 Synaptoso
34	40	46.5	206	4	AAU02639 Synaptoso
35	39	45.3	206	4	AAU00256 Synaptoso
36	39	45.3	206	4	AAU00266 Synaptoso
37	39	45.3	206	4	AAU00258 Synaptoso
38	39	45.3	206	4	AAU00262 Synaptoso
39	39	45.3	206	4	AAU00260 Synaptoso
40	39	45.3	206	4	AAU00257 Synaptoso
41	37	43.0	37	2	AAW30097 Neurotran
42	33	38.4	33	6	AAE36683 Goldfish
43	33	38.4	33	6	AAE36678 SNAP-25 p
44	27	31.4	49	4	AAW57386 Human bra
45	26	30.2	26	2	AAW30099 Neurotran

ALIGNMENTS

RESULT 1

AAB15584
ID AAB15584 standard; peptide; 86 AA.
XX
AC AAB15584;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #4.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
PN WO200064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES0000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
(LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
WPI; 2001-007091/01.
XX
New peptides containing amino acid sequences from known proteins for treatment of neurological disorders.
XX
Claim 16; Page 32-33; 40pp; Spanieh.
XX
The invention relates to new peptides comprising 3-30 contiguous amino acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated protein 25). The peptides AAB1581-B15586 represent examples of the peptides of the invention. The peptides have neuronal exocytosis inhibitory activity and are used for treatment of facial wrinkles and disorders and pathological neuronal exocytosis-mediated pathological disorders and alterations manifested e.g. by spasms and neurological and neurodegenerative disorders
XX
Sequence 86 AA;

```

Query Match      100.0%; Score 86; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.9e-80;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDERQMAISGGFIRVTVARENEEMDENLEQVSGILGNLRHMDMGNEIDTQNRQIDR 60
   |||||
DB 1 VDERQMAISGGFIRVTVARENEEMDENLEQVSGILGNLRHMDMGNEIDTQNRQIDR 60
   |||||

QY 61 INEKADSNKTRIDEANQKATKMLGSG 86
   |||||
DB 61 INEKADSNKTRIDEANQKATKMLGSG 86

RESULT 2
AAR86823
ID AAR86823 standard; peptide; 70 AA.
XX
AC AAR86823;
XX
XX 15-AUG-1996 (first entry)
XX
XX SNAP-25 residues 137-206.
XX
KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;
KW neurotransmitter; neurotoxin; botulinum; botulinum; cleavage; substrate;
KW antibody; detection; assay.
XX
OS Synthetic.
XX
PN WO9533850-A1.
XX
PD 14-DEC-1995.
XX
PF 02-JUN-1995; 95WO-GB001279.
XX
PR 03-JUN-1994; 94GB-0001138.
XX
XX (MTCR-) MICROBIOLOGICAL RES AUTHORITY.
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.
XX
XX Shone CC, Hallis B, James BAF, Quinn CP;
XX
XX WPI; 1996-040249/04.
XX
XX Assay for botulinum or tetanus toxin - by combining test cpd. with
PT substrate which is cleaved by the toxin, and antibody specific for the
PT cleaved but not uncleaved substrate.
XX
XX Example 4; Page 19; 48pp; English.
XX
XX The botulinum neurotoxins possess highly specific zinc-endopeptidase
CC activities within their light sub-units. Depending on the neurotoxin type
CC these act to cleave small proteins within the nerve cell which are
CC involved in neurotransmitter release. Antibodies are used in assays which
CC detect cleaved but not uncleaved substrate. Assays for botulinum types A
CC and E use the present sequence as a substrate. The sequence is SNAP-25
CC protein, residues 137-206
XX
SQ Sequence 70 AA;

Query Match      57.0%; Score 49; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.1e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
   |||||
DB 22 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 70
   |||||

RESULT 3
AAO15165
ID AAO15165 standard; peptide; 116 AA.

```

```

XX AAO15165;
AC
XX 02-SEP-2002 (first entry)
DT
XX
XX Clostridial neurotoxin protease substrate peptide 4.
DE
XX Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;
KW fluorescence resonant energy transfer assay; quenched-signal;
KW clostridial neurotoxin detection; food.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "S-fluoresceinyl-cysteine"
FT Cleavage-site 89..90
FT /note= "The peptide is cleaved between these two residues
FT by type E Clostridium botulinum neurotoxin"
FT Cleavage-site 106..107
FT /note= "The peptide is cleaved between these two residues
FT by type A Clostridium botulinum neurotoxin"
XX
PN WO200225284-A2.
XX
XX 28-MAR-2002.
PD
XX 25-SEP-2001; 2001WO-US030188.
PF
XX 25-SEP-2000; 2000US-0235050P.
PR
XX (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
PA
XX Schmidt JJ, Stafford RG;
PI
XX WPI; 2002-499829/53.
DR
XX Substrate useful in e.g. an assay for the protease activity of
PT clostridial neurotoxin, comprises modified peptide or protein.
XX
XX Claim 22; Page 16; 48pp; English.
XX
XX The invention comprises clostridial neurotoxin substrate peptides which
CC can serve as fluorescence resonant energy transfer assay (FRET) or
CC quenched-signal substrates in assays for the proteolytic activities of
CC clostridial neurotoxins. The invention further comprises Clostridium
CC botulinum neurotoxin substrate peptides that can serve as immobilised
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
CC activities of clostridial neurotoxins. The clostridial (including the
CC Clostridium botulinum) neurotoxin substrate peptides are useful for
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
CC or an environmental sample). The present amino acid sequence represents a
CC clostridial neurotoxin substrate peptide of the invention
XX
SQ Sequence 116 AA;

Query Match      57.0%; Score 49; DB 5; Length 116;
Best Local Similarity 100.0%; Pred. No. 3.3e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 86
   |||||
DB 67 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQKATKMLGSG 115
   |||||

RESULT 4
AAW30103
ID AAW30103 standard; peptide; 206 AA.
XX
AC AAW30103;
XX
XX 06-APR-1998 (first entry)
DT
XX

```

DE Synaptosomal associated protein.
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX Homo sapiens.
 XX WO9734620-A1.
 XX 25-SEP-1997.
 XX 18-MAR-1997; 97WO-US004393.
 XX 18-MAR-1996; 96US-0013599P.
 XX (REGC) UNIV CALIFORNIA.
 PA Montal M;
 PI WPI; 1997-479986/44.
 DR Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX Disclosure; Page 27-28; 61pp; English.
 CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 micromM, especially 0.25 micromM, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 5
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX AAW43426;
 AC
 XX 27-APR-1998 (first entry)
 DT Mouse synaptosomal-associated protein-25.
 DE
 XX Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 KW neurodegenerative disease; hormonal disorder; immunological disorder.
 XX Mus sp.
 OS

XX US5693476-A.
 XX 02-DEC-1997.
 XX 24-FEB-1995; 95US-00393985.
 XX 24-FEB-1995; 95US-00393985.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Scheller RH;
 PI WPI; 1998-031743/03.
 DR N-PSDE; AAV01554.
 XX Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 XX Disclosure; Col 67-72; 57pp; English.
 CC This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 6
 AAW79198
 ID AAW79198 standard; protein; 206 AA.
 XX AAW79198;
 AC
 XX 25-NOV-1998 (first entry)
 DT Mouse SNAP-25 polypeptide.
 DE
 XX Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;
 KW calcium-regulated secretion; secretory vesicle; secretory process; brain;
 KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;
 KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;
 KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
 KW immune system; antigen processing; immunomodulator; viral processing;
 KW central nervous system; vesicular release; affective disorder; human;
 KW anti-tumour application; membrane trafficking regulation; mouse.
 XX Mus sp.
 OS
 XX WO9838210-A2.
 PN 03-SEP-1998.
 PD 26-FEB-1998; 98WO-US003789.
 XX 26-FEB-1997; 97US-0039159P.
 PR

XX PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX PI Bean AJ, Scheller RH;
 XX PD WPI; 1998-481140/41.
 DR N-PSDB; AAV57558.
 XX
 XX New isolated Hrs-2 nucleotidase - used in assays to identify compounds
 PT capable of modulating calcium-regulatory secretion of secretory vesicles,
 PT such as in neurotransmitter release.
 XX
 XX Claim 16; Page 42-44; 55pp; English.
 XX
 XX This represents a mouse SNAP-25 polypeptide, a component of the protein
 CC polypeptides thought to underlie vesicle docking and fusion. The
 CC invention provides rat and human Hrs-2 polypeptides which are ATP-
 CC preferring nucleotidase that associate with SNAP-25. For identifying a
 CC compound capable of modulating calcium-regulated secretion of secretory
 CC vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2
 CC polypeptide, in the presence and absence of a test compound. The effect
 CC of the test compound on the extent of binding between the SNAP-25 and Hrs
 CC -2 polypeptides are measured and a compound is identified as effective if
 CC its measured effect on the extent of binding is above a threshold level.
 CC The products can be used for identifying drugs capable of affecting
 CC secretory processes, such as neurotransmitter release at the active zones
 CC or presynaptic membranes. Such drugs can be used for treating disorders
 CC or conditions of the central nervous system by selectively enhancing or
 CC inhibiting vesicular release in specific areas of the brain, including
 CC affective disorders (e.g. depression), disorders of thought (e.g.
 CC schizophrenia) and degenerative disorders (Parkinson's disease), as well
 CC as applications such as anaesthesia. The drugs can also be used
 CC therapeutically in other systems such as the endocrine system for
 CC treatment of hormonal imbalances, the immune system for intervention in
 CC antigen processing, secreted immunomodulators, and viral processing, as
 CC well as anti-tumour applications, such as regulation of membrane
 CC trafficking during rapid cell division
 XX
 XX Sequence 206 AA;

Query Match 57.0%; Score 49; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 7
 AAU00246
 ID AAU00246 standard; protein; 206 AA.
 XX
 XX AAU00246;
 XX
 XX 12-SEP-2001 (first entry)
 DE Synaptosomal-associated protein, SNAP25.
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mutagenic; PCR primer; mouse;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 XX Mus sp.

XX Key Location/Qualifiers
 FH Cleavage-site 180..191
 FT /note= "Peptide bond susceptible to cleavage by
 FT clostridial neurotoxin"
 FT Cleavage-site 197..198
 FT /note= "Peptide bonds susceptible to cleavage by
 FT

FT clostridial neurotoxin"

XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX

PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX Disclosure; Fig 8; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25. The sequence was used to create SNAP-25
 CC double/single point mutants and C-terminal deletion mutants used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)- attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state

XX Sequence 206 AA;

Query Match 57.0%; Score 49; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 8
 AAU00253
 ID AAU00253 standard; protein; 206 AA.
 XX
 XX AAU00253;
 XX
 XX 12-SEP-2001 (first entry)
 DE SNARE homologue, synaptosomal-associated protein, hSNAP25b.
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; hSNAP25b; human.
 XX
 XX Homo sapiens.

XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX N-PSDB; AAS00370.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX Disclosure; Fig 8; 131pp; English.
 XX The sequence represents the amino acid sequence of SNARE homologue,
 XX synaptosomal-associated membrane protein, hSNAP25b, used during analysis
 XX of SNAP-25. SNAP-25 mutants were used in a new method of treating a
 XX patient suffering from poisoning or at risk of poisoning by a clostridial
 XX toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive
 XX fusion protein)-attachment protein receptor) to a cell of the patient,
 XX where the SNARE is resistant to proteolysis by the toxin (toxin-resistant
 XX SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory
 XX SNARE). The protein can be used in a method of treating a patient in need
 XX of inhibition of SNARE-dependent exocytosis from a cell capable of
 XX performing SNARE-dependent exocytosis, comprises supplying a fragment,
 XX variant, fusion or derivative of a SNARE or an inhibitory SNARE to the
 XX cell of the patient. The toxin resistant or toxin inhibitory SNARE or a
 XX recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state
 XX Sequence 206 AA;
 XX Query Match 57.0%; Score 49; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLHRLMDMGNEIDTQNRQIDRIMEXKADSNKTRIDEANQRATMLGSG 86
 |||||
 Db 158 GNLHRLMDMGNEIDTQNRQIDRIMEXKADSNKTRIDEANQRATMLGSG 206
 |||||
 RESULT 9
 AAU00252
 ID AAU00252 standard; protein; 206 AA.
 XX AC AAU00252;
 XX 12-SEP-2001 (first entry)
 XX SNARE homologue, synaptosomal-associated protein, hSNAP25a.
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; hSNAP25a; human;
 XX N-ethylmaleimide-sensitive fusion;
 XX soluble NSF-attachment protein receptor.

XX OS Homo sapiens.
 XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX N-PSDB; AAS00369.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX Disclosure; Fig 8; 131pp; English.
 XX The sequence represents the amino acid sequence of SNARE homologue,
 XX synaptosomal-associated membrane protein, hSNAP25a, used during analysis
 XX of SNAP-25. SNAP-25 mutants were used in a new method of treating a
 XX patient suffering from poisoning or at risk of poisoning by a clostridial
 XX toxin, comprising supplying a SNARE (soluble (N-ethylmaleimide-sensitive
 XX fusion protein)-attachment protein receptor) to a cell of the patient,
 XX where the SNARE is resistant to proteolysis by the toxin (toxin-resistant
 XX SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory
 XX SNARE). The protein can be used in a method of treating a patient in need
 XX of inhibition of SNARE-dependent exocytosis from a cell capable of
 XX performing SNARE-dependent exocytosis, comprises supplying a fragment,
 XX variant, fusion or derivative of a SNARE or an inhibitory SNARE to the
 XX cell of the patient. The toxin resistant or toxin inhibitory SNARE or a
 XX recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state
 XX Sequence 206 AA;
 XX Query Match 57.0%; Score 49; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 XX Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLHRLMDMGNEIDTQNRQIDRIMEXKADSNKTRIDEANQRATMLGSG 86
 |||||
 Db 158 GNLHRLMDMGNEIDTQNRQIDRIMEXKADSNKTRIDEANQRATMLGSG 206
 |||||
 RESULT 10
 AAE36662
 ID AAE36662 standard; protein; 206 AA.
 XX AC AAE36662;
 XX 07-AUG-2003 (first entry)
 XX Human SNAP-25 protein.
 XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 XX tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 XX cosmetic.

XX OS Homo sapiens.
 XX PN WO2003020948-A2.
 XX PD 13-MAR-2003.
 XX PF 22-AUG-2002; 2002WO-US027145.
 XX PR 28-AUG-2001; 2001US-00942024.
 XX PA (ALLR) ALLERGAN INC.
 XX PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX DR WPI; 2003-290198/28.
 XX PT Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX PS Claim 6; Page 135-136; 168pp; English.
 XX CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is human
 CC SNAP-25 protein used in the invention
 XX SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 6; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHWMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 DB 158 GNLRHWMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 11
 AAE36667
 ID AAE36667 standard; protein; 206 AA.
 XX AC AAE36667;
 XX DT 07-AUG-2003 (first entry)
 XX DE Rat VAMP-2 protein.
 XX KW Rat; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT;
 KW tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical;
 KW cosmetic.
 XX OS Rattus sp.
 XX PN WO2003020948-A2.
 XX PR 01-NOV-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.

PD 13-MAR-2003.
 XX 22-AUG-2002; 2002WO-US027145.
 XX PR 28-AUG-2001; 2001US-00942024.
 XX PA (ALLR) ALLERGAN INC.
 XX PI Steward LE, Fernandez-Salas E, Aoki KR;
 XX DR WPI; 2003-290198/28.
 XX PT Botulinum serotype A/E substrate useful for assaying protease activity of
 PT botulinum toxins, comprises donor fluorophore, acceptor and a clostridial
 PT toxin recognition sequence that includes a cleavage site.
 XX PS Disclosure; Page 137-138; 168pp; English.
 XX CC The present invention relates to novel clostridium toxin substrates. The
 CC invention further relates to botulinum serotype A/E (BoNT/A/E) substrates
 CC which comprise a donor fluorophore, an acceptor having an absorbance
 CC spectrum overlapping the emission spectrum of the donor fluorophore and a
 CC BoNT A or BoNT/E recognition sequence comprising a cleavage site, where
 CC the cleavage site intervenes between the donor fluorophore and acceptor
 CC and under the appropriate conditions, the resonance energy transfer is
 CC exhibited between the donor and acceptor. Natural targets of clostridium
 CC neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences
 CC of the invention are useful in assaying for the protease activity of any
 CC clostridial toxin including botulinum toxins of all serotypes and tetanus
 CC toxins (TeNT) in a sample including bacterial, baculoviral and yeast
 CC lysate, raw, cooked or processed foods, beverages, animal feed, soil
 CC samples, water samples, cosmetics, tissue samples and beverage or food
 CC samples. They are useful to assay a sample from a human or animal, for
 CC e.g., exposed to clostridial toxin or having one or more symptoms of a
 CC clostridial toxin, to follow activity during production and purification
 CC of clostridial toxin and to assay formulated clostridial toxin products
 CC including pharmaceuticals and cosmetics. The present sequence is rat VAMP
 CC -2 protein used in the invention
 XX SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 6; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHWMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 DB 158 GNLRHWMALDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206
 RESULT 12
 ADE54280
 ID ADE54280 standard; protein; 206 AA.
 XX AC ADE54280;
 XX DT 29-JAN-2004 (first entry)
 XX DE Rat Protein BAA20151, SEQ ID NO 83.
 XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX OS Rattus norvegicus.
 XX PN WO2003016475-A2.
 XX PD 27-FEB-2003.
 XX PF 14-AUG-2002; 2002WO-US025765.
 XX PR 14-AUG-2001; 2001US-0312147P.
 XX PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.
 XX (GEOH) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20151.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially regulated in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKTIRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKTIRIDEANQRATKMLGSG 206
 RESULT 13
 ADE54288
 ID ADE54288 standard; protein; 206 AA.
 XX ADE54288;
 AC ADE54288;
 XX 29-JAN-2004 (first entry)
 DT Rat Protein BAA20152, SEQ ID NO 91.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 KW Rattus norvegicus.
 OS WO2003016475-A2.
 XX 27-FEB-2003.
 PD Rattus norvegicus.
 XX

PF 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 XX (GEOH) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; BAA20152.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 1017pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 206 AA;
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKTIRIDEANQRATKMLGSG 86
 Db 158 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKTIRIDEANQRATKMLGSG 206
 RESULT 14
 ADE54276
 ID ADE54276 standard; protein; 206 AA.
 XX ADE54276;
 AC ADE54276;
 XX 29-JAN-2004 (first entry)
 DT Rat Protein BAA20151, SEQ ID NO 79.
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 KW Rattus norvegicus.
 OS WO2003016475-A2.
 XX 27-FEB-2003.
 PD Rattus norvegicus.
 XX

PN WC2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; BAA20151.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 101pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKRTRIDEANQRATKMLGSG 86
 DB 158 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKRTRIDEANQRATKMLGSG 206
 RESULT 15
 ADE54290
 ID ADE54290 standard; protein; 206 AA.
 XX ADE54290;
 XX AC
 XX 29-JAN-2004 (first entry)
 DT Human Protein P13795, SEQ ID NO 93.
 XX Human; pain; neuronal tissue; gene therapy;
 XX AC
 XX KW

KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 XX GENBANK; P13795.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Claim 1; Page; 101pp; English.
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
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 CC that increases or decreases the expression of the polynucleotide sequence
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
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 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
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 CC the specification) which is differentially expressed during pain. Note:
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 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 206 AA;
 SQ
 Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKRTRIDEANQRATKMLGSG 86
 DB 158 GNLRHMDMGNEIDTQNRQIDRIEAKDSNKRTRIDEANQRATKMLGSG 206
 RESULT 16
 ADE54282
 ID ADE54282 standard; protein; 206 AA.
 XX ADE54282;
 XX AC
 XX

DT 29-JAN-2004 (first entry)
XX DE Rat Protein BAA20151, SEQ ID NO 85.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX OS
XX WO2003016475-A2.
XX PD 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX PF
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; BAA20151.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
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CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
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CC The sequence data for this patent did not form part of the printed
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CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 17
ADE54274

ID ADE54274 standard; protein; 206 AA.
XX AC ADE54274;
XX
XX 29-JAN-2004 (first entry)
XX DT
XX DE Rat Protein BAA20151, SEQ ID NO 77.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX OS
XX WO2003016475-A2.
XX PN
XX 27-FEB-2003.
XX PD
XX 14-AUG-2002; 2002WO-US025765.
XX PF
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; BAA20151.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
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CC the expression of a polynucleotide sequence which is differentially
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CC polynucleotides, a method for producing a pharmaceutical composition, a
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CC pain and a pharmaceutical composition comprising the one or more
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CC pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
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XX Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 206

RESULT 18
ADE54286
ID ADE54286 standard; protein; 206 AA.

XX AC ADE54286;
XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P13795, SEQ ID NO 89.

XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX KW WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX KW (GHEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX XX Woolf C, D'urso D, Befort K, Costigan M;

XX XX WPI; 2003-268312/26.

XX DR GENEANK; P13795.

XX XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PT PT Claim 1; Page; 1017pp; English.

PS The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

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CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

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CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

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CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

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CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

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CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

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CC therapy). The sequence presented is a human protein (shown in Table 2 of

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CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 206 AA;

XX Query Match 57.0%; Score 49; DB 7; Length 206;

XX Best Local Similarity 100.0%; Pred. No. 5.5e-42;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GNLRHMDMGNEIDTONQIDRIMEKADSNKTRIDEANQRTKMLGSG 86

Db 158 GNLRHMDMGNEIDTONQIDRIMEKADSNKTRIDEANQRTKMLGSG 206

RESULT 19

ADE54284

XX ID ADE54284 standard; protein; 206 AA.

XX AC ADE54284;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein BAA20152, SEQ ID NO 87.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX KW WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX KW (GHEO) GEN HOSPITAL CORP.

XX PA (FARB) BAYER AG.

XX XX Woolf C, D'urso D, Befort K, Costigan M;

XX XX WPI; 2003-268312/26.

XX DR GENEANK; BAA20152.

XX XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PT PT Claim 1; Page; 1017pp; English.

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XX

SQ Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 206

RESULT 20

ADBS4272
ID ADE54272 standard; protein; 206 AA.

AC ADE54272;

DT 29-JAN-2004 (first entry)

DE Rat Protein BAA20151, SEQ ID NO 75.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; BAA20151.

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CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
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CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
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SQ Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
Best Local Similarity 100.0%; Pred. No. 5.5e-42;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 86
Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQRTKMLGSG 206

RESULT 21

ADBS4278

ID ADE54278 standard; protein; 206 AA.

AC ADE54278;

DT 29-JAN-2004 (first entry)

DE Rat Protein BAA20151, SEQ ID NO 81.

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; BAA20151.

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CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
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CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
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 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 206 AA;

Query Match 57.0%; Score 49; DB 7; Length 206;
 Best Local Similarity 100.0%; Pred. No. 5.5e-42;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMALDGMNEIDTQNRQIDRIMEKADSNKTRIDEANORATKM 86
 |||||
 DB 158 GNLRLMALDGMNEIDTQNRQIDRIMEKADSNKTRIDEANORATKM 206

RESULT 22

AAU02640
 ID AAU02640 standard; protein; 206 AA.

AC AAU02640;

XX 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant L203A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 203 /note= "Wild-type Leu substituted by Ala"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant L203A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprising supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE

CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 206 AA;

Query Match 52.3%; Score 45; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 6.9e-38;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMALDGMNEIDTQNRQIDRIMEKADSNKTRIDEANORATKM 82
 |||||
 DB 158 GNLRLMALDGMNEIDTQNRQIDRIMEKADSNKTRIDEANORATKM 202

RESULT 23

AAU02638

ID AAU02638 standard; protein; 206 AA.

XX AAU02638;

XX 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant M202A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 202 /note= "Wild-type Met substituted by Ala"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant M202A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-

OS Mus sp.
OS Synthetic.
XX WO200118038-A2.
XX 15-MAR-2001.
XX 18-AUG-2000; 200WO-GB003196.
PF 20-AUG-1999; 99US-0149993P.
PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
FA WPI; 2001-226739/23.
PI Treating a patient suffering from poisoning or at risk of poisoning by a
XX clostridial toxin, e.g. botulism, comprises administering a toxin-
XX resistant or toxin-inhibitory SNARE.
XX Example 1; Page; 131pp; English.
XX The sequence represents the amino acid sequence of synaptosomal-
CC

WPI; 2002-499829/53.

Query Match	47.7%;	Score 41;	DB 4;	Length 198;
Best Local Similarity	100.0%;	Pred. No. 8.5e-34;		

PT Substrate useful in e.g. an assay for the protease activity of
 PT clostridial neurotoxin, comprises modified peptide or protein.
 XX
 PS Claim 28; Page 17; 48pp; English.
 XX
 CC The invention comprises clostridial neurotoxin substrate peptides which
 CC can serve as fluorescence resonant energy transfer assay (FRET) or
 CC quenched-signal substrates in assays for the proteolytic activities of
 CC clostridial neurotoxins. The invention further comprises Clostridium
 CC botulinum neurotoxin substrate peptides that can serve as immobilised
 CC substrates (i.e. bound to a solid phase) in assays for the proteolytic
 CC activities of clostridial neurotoxins. The clostridial (including the
 CC Clostridium botulinum) neurotoxin substrate peptides are useful for
 CC detecting the presence of clostridial neurotoxins in a sample (e.g. food
 CC or an environmental sample). The present amino acid sequence represents a
 CC clostridial neurotoxin substrate peptide of the invention
 XX
 SQ Sequence 116 AA;
 Query Match 46.5%; Score 40; DB 5; Length 116;
 Best Local Similarity 100.0%; Pred. No. 5.6e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRLMWDGNEIDTQNRQIDRIMKADSNKTRIDEANQ 77
 Db 67 GNLRLMWDGNEIDTQNRQIDRIMKADSNKTRIDEANQ 106
 RESULT 26
 AAU00263
 ID AAU00263 standard; protein; 199 AA.
 AC AAU00263;
 XX
 DT 12-SEP-2001 (first entry)
 DE Synaptosomal-associated protein, SNAP25, mutant 1-199(R198T).
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 XX W0200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199(R198T), used in a new method of

CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 199 AA;
 Query Match 46.5%; Score 40; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 9e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRLMWDGNEIDTQNRQIDRIMKADSNKTRIDEANQ 77
 Db 158 GNLRLMWDGNEIDTQNRQIDRIMKADSNKTRIDEANQ 197
 RESULT 27
 AAU00264
 ID AAU00264 standard; protein; 200 AA.
 AC AAU00264;
 XX
 DT 12-SEP-2001 (first entry)
 DE Synaptosomal-associated protein, SNAP25, mutant 1-200(R198T).
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 XX
 XX W0200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-
PT resistant or toxin-inhibitory SNARE.

Example 1; Page: 131pp; English.

The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant 1-200(R198T), used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis, comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of critical state. Note: The present sequence is not shown in the specification but is derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246).

XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX DR WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 XX PT clostridial toxin, e.g. botulinum, comprises administering a toxin-
 XX PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 XX CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 XX CC creating a patient suffering from poisoning or at risk of poisoning by a
 XX CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX CC ethylmaleimide-sensitive fusion protein))-attachment protein receptor) to
 XX CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX CC or a recombinant polynucleotide encoding the SNARE is useful in the
 XX CC manufacture of a medicament for the treatment of a patient suffering from
 XX CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX CC botulinum or tetanus. The fragment, variant, fusion or derivative of a
 XX CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX CC either of these SNARE polypeptides are useful in the manufacture of
 XX CC medicament for the treatment of a patient in need of inhibition of SNARE-
 XX CC dependent exocytosis from a cell capable of performing SNARE-dependent
 XX CC exocytosis. The method of treatment is relatively fast, thus alleviating
 XX CC the symptoms when most severe and taking the patient out of critical
 XX CC state. Note: The present sequence is not shown in the specification but
 XX CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX CC AAU00246)
 XX SQ Sequence 202 AA;
 Query Match 46.5%; Score 40; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 9.1e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLHRWALDGMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLHRWALDGMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197
 RESULT 30
 AAU02636
 ID AAU02636 standard; protein; 203 AA.
 XX AC AAU02636;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, mutant 1-203(R198T).
 XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX KW toxin-inhibitory SNARE; botulinum; tetanus; SNARE-dependent exocytosis;
 XX KW synaptosomal-associated protein; mouse; mutant; mteuin;
 XX KW N-ethylmaleimide-sensitive fusion protein;
 XX KW soluble NSF-attachment protein receptor.
 XX OS Mus sp.

OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 XX PN 15-MAR-2001.
 XX PD 18-AUG-2000; 2000WO-GB003196.
 XX PF 20-AUG-1999; 99US-0149993P.
 XX PR (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PA Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX PI WPI; 2001-226739/23.
 XX DR Treating a patient suffering from poisoning or at risk of poisoning by a
 XX DR clostridial toxin, e.g. botulinum, comprises administering a toxin-
 XX DR resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 XX CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 XX CC treating a patient suffering from poisoning or at risk of poisoning by a
 XX CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX CC ethylmaleimide-sensitive fusion protein))-attachment protein receptor) to
 XX CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX CC or a recombinant polynucleotide encoding the SNARE is useful in the
 XX CC manufacture of a medicament for the treatment of a patient suffering from
 XX CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX CC botulinum or tetanus. The fragment, variant, fusion or derivative of a
 XX CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX CC either of these SNARE polypeptides are useful in the manufacture of
 XX CC medicament for the treatment of a patient in need of inhibition of SNARE-
 XX CC dependent exocytosis from a cell capable of performing SNARE-dependent
 XX CC exocytosis. The method of treatment is relatively fast, thus alleviating
 XX CC the symptoms when most severe and taking the patient out of critical
 XX CC state. Note: The present sequence is not shown in the specification but
 XX CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX CC AAU00246)
 XX SQ Sequence 203 AA;
 Query Match 46.5%; Score 40; DB 4; Length 203;
 Best Local Similarity 100.0%; Pred. No. 9.2e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLHRWALDGMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 DB 158 GNLHRWALDGMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197
 RESULT 31
 AAU00261
 ID AAU00261 standard; protein; 206 AA.
 XX AC AAU00261;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, mutant R198A.
 XX DE

KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Ala"
 XX W0200118038-A2.

XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T/L203A, used in a new method of treating
 CC a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX SQ Sequence 206 AA;
 Query Match 46.5%; Score 40; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLHMDMGNEIDTQRIIDIMEKADSNKTRIDEANQ 77
 DB 158 GNLRLHMDMGNEIDTQRIIDIMEKADSNKTRIDEANQ 197

RESULT 32
 AAU02171
 ID AAU02171 standard; protein; 206 AA.

XX AC AAU02171;
 XX 12-SEP-2001 (first entry)
 XX Synaptosomal-associated protein, SNAP25, mutant R198T/L203A.
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 FT Misc-difference 203
 FT /note= "Wild-type Leu substituted by Ala"
 XX W0200118038-A2.

XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T/L203A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX SQ Sequence 206 AA;

Query Match 46.5%; Score 40; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMADMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 XX |||||
 Db 158 GNLRLMADMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 33

AAU00259
 ID AAU00259 standard; protein; 206 AA.

AC AAU00259;

XX 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant R198T.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T used in a new method of treating
 CC a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC a medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see

CC AAU00246)

XX Sequence 206 AA;

XX Query Match 46.5%; Score 40; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 9,3e-33;
 XX Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 GNLRLMADMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77

Db 158 GNLRLMADMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 34

AAU02639
 ID AAU02639 standard; protein; 206 AA.

AC AAU02639;

XX 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant R198T/M202A.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Thr"

FT Misc-difference 202

FT /note= "Wild-type Met substituted by Ala"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant R198T/M202A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from

CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 206 AA;
 SQ

Query Match 46.5%; Score 40; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.3e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 77
 |||||
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEANQ 197

RESULT 35
 AAU00256
 ID AAU00256 standard; protein; 206 AA.
 XX
 AC AAU00256;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant Q197A/R198A.
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.

XX
 PH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Ala"
 FT
 XX WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX
 PR 20-AUG-1999; 99US-0149993P.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 DR WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 131pp; English.
 XX

CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant Q197A/R198A, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the

CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of SNARE-
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 206 AA;
 SQ

Query Match 45.3%; Score 39; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.9e-32;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 |||||
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 36
 AAU00266
 ID AAU00266 standard; protein; 206 AA.
 XX
 AC AAU00266;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant Q197K/R198H.
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.

XX
 PH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Lys"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by His"
 FT
 XX WO200118038-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 18-AUG-2000; 2000WO-GB003196.
 XX
 PR 20-AUG-1999; 99US-0149993P.
 XX
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 DR WPI; 2001-226739/23.
 XX

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX PS Example 1; Page; 131pp; English.

XX CC The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant Q197K/R198W, used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis, comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of a medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of critical state. Note: The present sequence is not shown in the specification but is derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246)

XX CC Sequence 206 AA;

Qy 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 |||||
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 37

AAU00258

ID AAU00258 standard; protein; 206 AA.

AC AAU00258;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant Q197W/R198W.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis; synaptosomal-associated protein; mouse; mutant; mutein;

KW N-ethylmaleimide-sensitive fusion protein;

XX soluble NSF-attachment protein receptor.

OS Mus sp.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 197

FT /note= "Wild-type Gln substituted by Trp"

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Trp"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, e.g. botulism, comprises administering a toxin-resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-associated protein, SNAP25, mutant Q197W/R198W, used in a new method of treating a patient suffering from poisoning or at risk of poisoning by a clostridial toxin, comprising supplying a SNARE (soluble N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to a cell of the patient, where the SNARE is resistant to proteolysis by the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin (toxin-inhibitory SNARE). The protein can be used in a method of treating a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis, comprises supplying a fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE to the cell of the patient. The toxin resistant or toxin inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is useful in the manufacture of a medicament for the treatment of a patient suffering from poisoning or at risk of poisoning by clostridial toxin, e.g. from botulism or tetanus. The fragment, variant, fusion or derivative of a SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding either of these SNARE polypeptides are useful in the manufacture of a medicament for the treatment of a patient in need of inhibition of SNARE-dependent exocytosis from a cell capable of performing SNARE-dependent exocytosis. The method of treatment is relatively fast, thus alleviating the symptoms when most severe and taking the patient out of critical state. Note: The present sequence is not shown in the specification but is derived from the mouse SNAP-25 sequence given in figure 8 (see AAU00246)

XX CC Sequence 206 AA;

Qy 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 |||||
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 38

AAU00262

ID AAU00262 standard; protein; 206 AA.

AC AAU00262;

DT 12-SEP-2001 (first entry)

DE Synaptosomal-associated protein, SNAP25, mutant Q197K/R198K.

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE; toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis; synaptosomal-associated protein; mouse; mutant; mutein;

KW N-ethylmaleimide-sensitive fusion protein;

XX soluble NSF-attachment protein receptor.

OS Mus sp.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 197

FT /note= "Wild-type Gln substituted by Lys"

FT Misc-difference 198

FT /note= "Wild-type Arg substituted by Lys"

XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX The sequence represents the amino acid sequence of synaptosomal-
 XX associated protein, SNAP25, mutant Q197X/R198K, used in a new method of
 XX treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX or a recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state. Note: The present sequence is not shown in the specification but
 XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX AAU00246)
 XX Sequence 206 AA;
 XX Query Match 45.3%; Score 39; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 9.9e-32;
 XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
 RESULT 39
 AAU00260
 ID AAU00260 standard; protein; 206 AA.
 XX AAU00260;
 AC AAU00260;
 XX 12-SEP-2001 (first entry)
 DT Synaptosomal-associated protein, SNAP25, mutant Q197A.
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 197
 FT /note= "Wild-type Gln substituted by Ala"
 XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX The sequence represents the amino acid sequence of synaptosomal-
 XX associated protein, SNAP25, mutant Q197A, used in a new method of
 XX treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, comprising supplying a SNARE (soluble (N-
 XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX or a recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state. Note: The present sequence is not shown in the specification but
 XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX AAU00246)
 XX Sequence 206 AA;
 XX Query Match 45.3%; Score 39; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 9.9e-32;
 XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 Db 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196
 RESULT 40
 AAU00257
 ID AAU00257 standard; protein; 206 AA.
 XX AAU00257;
 AC AAU00257;
 XX 12-SEP-2001 (first entry)
 DT Synaptosomal-associated protein, SNAP25, mutant Q197A.
 DE SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

DE Synaptosomal-associated protein, SNAP25, mutant Q197A/R198K.
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 197
 FT /note= "Wild-type Gln substituted by Ala"
 FT Misc-difference 198
 FT /note= "Wild-type Arg substituted by Lys"
 FT
 XX WC200118038-A2.
 FN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 PI
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 FT clostridial toxin, e.g. botulism, comprises administering a toxin-
 FT resistant or toxin-inhibitory SNARE.
 FT
 XX Example 1; Page, 131pp; English.
 PS
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant Q197A/R198K, used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU000246)
 XX
 SQ Sequence 206 AA;
 Query Match 45.3%; Score 39; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 9.9e-32;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 38 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 76
 DB 158 GNLRHMDMGNEIDTQNRQIDRIMEKADSNKTRIDEAN 196

RESULT 41
 AAW30097
 ID AAW30097 standard; peptide; 37 AA.
 XX
 AC AAW30097;
 DT 06-APR-1998 (first entry)
 XX
 DE Neurotransmitter secretion inhibitor #1.
 XX
 KW Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX
 PN WC9734620-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US004393.
 XX
 PR 18-MAR-1996; 96US-0013599P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Montal M;
 XX
 DR WPI; 1997-479986/44.
 XX
 PT Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neurotransmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX
 PS Claim 1; Page 30; 61pp; English.
 CC This sequence corresponds to residues 170-206 of the human 25 kD
 CC synaptosomal associated protein (SNAP-25), and is an inhibitory agent of
 CC the invention. The agents of the invention inhibit secretion of
 CC neurotransmitter from neuronal cells and is an excitation-secretory
 CC uncoupling peptide (I) of at least 20 amino acids (aa) all of which
 CC correspond substantially to any one of AAW30097-W30102, or more generally
 CC any (I) that inhibits 50% of catecholamine secretion from bovine
 CC chromaffin cells at a concentration of 10 microm, especially 0.25 microm,
 CC or less. (I) are used, as a replacement for Clostridium toxin, to inhibit
 CC release of neurotransmitters from synaptic vesicles, specifically for
 CC reducing muscle spasticity. Also (I) may be labelled to allow in vivo
 CC imaging of intracellular distribution of (I). Compounds for delivering
 CC the drug to neural cells provide targeted drug delivery, e.g. of
 CC substance P to brain tumours for induction of apoptosis. Unlike the
 CC neurotoxins, (I) are not toxic or immunogenic and are more readily
 CC available. Their therapeutic effect lasts for several days or weeks, so
 CC lower doses or less frequent treatments are required
 XX
 SQ Sequence 37 AA;
 Query Match 43.0%; Score 37; DB 2; Length 37;
 Best Local Similarity 100.0%; Pred. No. 2.4e-30;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 50 EIDTQNRQIDRIMEKADSNKTRIDEANQRTKQLGSG 86
 DB 1 EIDTQNRQIDRIMEKADSNKTRIDEANQRTKQLGSG 37
 RESULT 42
 AAE36683
 ID AAE36683 standard; peptide; 33 AA.
 XX
 AC AAE36683;
 XX

DT 07-AUG-2003 (first entry)
 XX Goldfish SNAP-25B peptide.
 XX
 XX Goldfish; clostridium toxin; protease activity; botulinum toxin; BoNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; TeNT; cosmetic.
 KW Carassius auratus.
 XX
 XX Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 XX
 XX WO2003020948-A2.
 PN
 XX 13-MAR-2003.
 XX
 XX 22-AUG-2002; 2002WO-US027145.
 XX
 XX 28-AUG-2001; 2001US-00942024.
 PR
 XX (ALLR) ALLERGAN INC.
 PA
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX WPI; 2003-290198/28.
 DR
 XX Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
 PT
 XX Disclosure; Page 42; 168pp; English.
 PS
 XX The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BoNT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is goldfish SNAP-25B peptide used in the invention
 CC
 XX Sequence 33 AA;
 SQ
 Query Match 38.4%; Score 33; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.7e-26;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 DB 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33
 RESULT 43
 AAE36678
 ID AAE36678 standard; peptide; 33 AA.

XX AAE36678;
 XX
 XX 07-AUG-2003 (first entry)
 XX
 XX SNAP-25 peptide.
 XX
 XX Human; clostridium toxin; protease activity; botulinum toxin; BoNT; TeNT; tetanus toxin; VAMP; synaptobrevin; SNAP-25; syntaxin; pharmaceutical; cosmetic; mouse; rat.
 KW
 KW Homo sapiens.
 XX Mus musculus.
 OS Rattus sp.
 XX
 XX Key Location/Qualifiers
 FT Cleavage-site 7..8 /note= "BoNT/E sensitive cleavage site"
 FT Cleavage-site 24..25 /note= "BoNT/A sensitive cleavage site"
 FT Cleavage-site 25..26 /note= "BoNT/C sensitive cleavage site"
 XX
 XX WO2003020948-A2.
 PN
 XX 13-MAR-2003.
 XX
 XX 22-AUG-2002; 2002WO-US027145.
 XX
 XX 28-AUG-2001; 2001US-00942024.
 PR
 XX (ALLR) ALLERGAN INC.
 PA
 XX Steward LE, Fernandez-Salas E, Aoki KR;
 PI
 XX WPI; 2003-290198/28.
 DR
 XX Botulinum serotype A/E substrate useful for assaying protease activity of botulinum toxins, comprises donor fluorophore, acceptor and a clostridial toxin recognition sequence that includes a cleavage site.
 PT
 XX Disclosure; Page 42; 168pp; English.
 PS
 XX The present invention relates to novel clostridium toxin substrates. The invention further relates to botulinum serotype A/E (BoNT/A/E) substrates which comprise a donor fluorophore, an acceptor having an absorbance spectrum overlapping the emission spectrum of the donor fluorophore and a BoNT A or BoNT/E recognition sequence comprising a cleavage site, where the cleavage site intervenes between the donor fluorophore and acceptor and under the appropriate conditions, the resonance energy transfer is exhibited between the donor and acceptor. Natural targets of clostridium neurotoxins include VAMP (synaptobrevin), SNAP-25 and syntaxin. Sequences of the invention are useful in assaying for the protease activity of any clostridial toxin including botulinum toxins of all serotypes and tetanus toxins (TeNT) in a sample including bacterial, baculoviral and yeast lysate, raw, cooked or processed foods, beverages, animal feed, soil samples, water samples, cosmetics, tissue samples and beverage or food e.g., exposed to clostridial toxin or having one or more symptoms of a clostridial toxin, to follow activity during production and purification of clostridial toxin and to assay formulated clostridial toxin products including pharmaceuticals and cosmetics. The present sequence is SNAP-25 peptide used in the invention
 CC
 XX Sequence 33 AA;
 SQ
 Query Match 38.4%; Score 33; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 2.7e-26;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 86
 DB 1 QNRQIDRIMEKADSNKTRIDEANQRATKMLGSG 33

Fri Mar 5 07:11:12 2004

bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction; synapticosomal associated protein; SNAP-25.

KW

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RESULT 44

AAW57386

ID AAW57386 standard; protein; 49 AA.

AC AAW57386;

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Result No.	Score	Query Match	Length	DB ID	Description
					%
1	62	100.0	206	13	Q8AXM2
2	62	100.0	206	13	Q8AXM1
3	57	91.9	18	6	Q3TRF1
4	45	72.6	794	5	Q7YR86
5	44	71.0	55	13	O93580
6	44	71.0	203	13	O93579
7	44	71.0	252	16	O99YW2
8	44	71.0	252	16	O8KG61
9	44	71.0	701	11	Q7TSZ7
10	42	67.7	1034	10	Q93X69
11	41	66.1	201	16	O88DN0
12	41	66.1	253	11	O9WV62
13	41	66.1	315	9	Q3G050
14	41	66.1	480	17	Q9UYW5
15	41	66.1	664	17	QHNM61
16	41	66.1	698	16	O8XQ01
					Q8AXM2 xenopus lae
					Q8AXM1 xenopus lae
					Q3TRF1 bos taurus
					Q7YR86 cryptospori
					O93580 brachydanio
					O93579 brachydanio
					O99YW2 streptococc
					O8KG61 streptococc
					Q7TSZ7 mus musculus
					Q93X69 oryza sativ
					O88DN0 pseudomonas
					O9WV62 rattus norv
					Q3G050 phage phihm
					Q9UYW5 pyrococcus
					QHNM61 halobacteri
					O8XQ01 ralstonia s

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP25B (Hypothetical protein).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 CX NCBI_TaxID=8355;
 RN [1]
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kolk S.M., Groffen A.J.A., Tuinhouf R., Verhage M., Roubos E.W.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Staptchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF335587; AA013789.1; -;
 DR EMBL; BC055981; AAH55981.1; -;
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR00727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; T_SNARE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;

Query Match 100.0%; Score 62; DB 13; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELEMORRADOLA 13
 Db |||||
 10 ELEMORRADOLA 22

RESULT 3
 Q9TRF1

ID Q9TRF1 PRELIMINARY; PRT; 18 AA.
 AC Q9TRF1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25
 DE (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=93374072; PubMed=8365494;
 RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,
 RA Abe T.;
 RL FEBS Lett. 330:236-240 (1993).
 SQ SEQUENCE 18 AA; 2120 MW; 371FC93766C4A7BB CRC64;

Query Match 91.9%; Score 57; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEEMORRADOLA 13
 Db |||||
 1 LEEMORRADOLA 12

RESULT 4

ID Q7YV86 PRELIMINARY; PRT; 794 AA.
 AC Q7YV86;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Asparagine-rich protein, possible.
 GN MBP390.
 OS Cryptosporidium parvum.
 CC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 CC Cryptosporidiidae; Cryptosporidium.
 CX NCBI_TaxID=5807;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Iowa;
 RA Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M.,
 RA Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
 RT "Integrated mapping, chromosomal sequencing and sequence analysis of
 RT Cryptosporidium parvum.";
 RL Genome Res. 0:0-0 (2003).
 DR EMBL; BX538351; CAD98599.1; -;
 SQ SEQUENCE 794 AA; 92848 MW; 37E6DF58F62A5358 CRC64;

Query Match 72.6%; Score 45; DB 5; Length 794;
 Best Local Similarity 61.5%; Pred. No. 71;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ELEMORRADOLA 13
 Db |||||
 777 BIELQORDELA 789

RESULT 5

O93580 PRELIMINARY; PRT; 55 AA.
 ID O93580
 AC O93580;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Synaptosome-associated protein 25.2 (Fragment).
 GN SNAP25B OR SNAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=9057281; PubMed=9841147;
 RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Lathammer D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage";
 RL J. Neurosci. Res. 54:563-573 (1998).
 DR EMBL; AF091595; AAC64290.1; -;
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 FT NON TER 55 55
 SQ SEQUENCE 55 AA; 6200 MW; 7ABBE9C2D3590AB9 CRC64;
 Query Match 71.0%; Score 44; DB 13; Length 55;
 Best Local Similarity 75.0%; Pred. No. 8.4;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMORRADQL 12
 Db 10 ELNDMQARADQL 21
 RESULT 6
 O93579
 ID O93579 PRELIMINARY; PRT; 203 AA.
 AC O93579;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SYNAPTOSOME-associated protein 25.2 (SYNAPTOSOME associated protein
 DE 25.2).
 GN SNAP25B OR SNAP.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]_SEQUENCE FROM N.A.
 RP Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Lathammer D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish;
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage";
 RL J. Neurosci. Res. 010-0(1998).
 DR EMBL; AF091594; AAC64290.1; -;
 DR EMBL; AF091596; AAC73007.1; -;
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t SNARE; 2.
 DR PROSITE; PS0192; T SNARE; 2.
 SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;
 Query Match 71.0%; Score 44; DB 13; Length 203;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMORRADQL 12
 Db 10 ELNDMQARADQL 21
 RESULT 7
 Q99YW2
 ID Q99YW2 PRELIMINARY; PRT; 252 AA.
 AC Q99YW2;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cell-division initiation protein (Septum placement).
 GN DIVIVAS OR SPY1514 OR SPYM18_1532.
 OS Streptococcus pyogenes, and
 OS Streptococcus pyogenes, and
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314, 186103;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN-SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [2]_SEQUENCE FROM N.A.
 RP STRAIN-WGAS8232 / Serotype M18;
 RX MEDLINE=21927593; PubMed=11917108;
 RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
 RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
 RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
 RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
 RT "Genome sequence and comparative microarray analysis of serotype M18
 RT group A Streptococcus strains associated with acute rheumatic fever
 RT outbreaks";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
 DR EMBL; AE006585; AAK34310.1; -;
 DR EMBL; AE010088; AAL98100.1; -;
 DR InterPro; IPR007793; DivIVA.
 DR Pfam; PF05103; DivIVA; 1.
 KW Complete proteome.
 SQ SEQUENCE 252 AA; 28934 MW; EB8BC08994B2CDC CRC64;
 Query Match 71.0%; Score 44; DB 16; Length 252;
 Best Local Similarity 72.7%; Pred. No. 35;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ELEMORRADQL 11
 Db 208 ELELQRRVDE 218
 RESULT 8
 Q8KGS1
 ID Q8KGS1 PRELIMINARY; PRT; 252 AA.
 AC Q8KGS1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative cell-division initiation protein (Septum placement).
 GN DIVIVA OR SPYM3_1167 OR SP80695.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 RN [1]_SEQUENCE FROM N.A.
 RP STRAIN-WGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=1212206;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).

<p> [2] RN SEQUENCE FROM N.A. RC STRAIN=SSI-1 / Serotype M3; RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A., RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M., RA Hayashi H., Hamada S. RT "The genome of invasive Streptococcus pyogenes; a comparative analysis RT of S. pyogenes SSI-1, SF370 and MGAS8232."; RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases. RL EMBL; AE014159; AAM79774.1; -. DR EMBL; AP005143; BAC63790.1; -. DR InterPro: IPR007793; DivIVA. DR Pfam; PF05103; DivIVA; 1. SQ Hypothetical protein; Complete proteome. KW SEQUENCE 252 AA; 28938 MW; E88BC0894AB29C8 CRC64; </p>	<p> Query Match 71.0%; Score 44; DB 16; Length 252; Best Local Similarity 72.7%; Pred. No. 35; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0; </p>
<p> QY 1 ELEEMORRADQ 11 : : : Db 208 ELEELQRRVDE 218 </p>	
<p> RESULT 9 Q7TSZ7 PRELIMINARY; PRT; 701 AA. </p>	
<p> AC Q7TSZ7 ID 01-OCT-2003 (TrEMBLrel. 25, Created) DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) DE KifA protein. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TaxID=10090; [1] RN SEQUENCE FROM N.A. RC STRAIN=C57BL/6; TISSUE=Brain; RX MEDLINE=22388257; PubMed=12477932; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Fahey J., Hellon E., Kettman M., Maman A., Rodrigues S., Sanchez A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., RA Jones S.J., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."; RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases. RL EMBL; BC052707; AAH52707.1; -. SQ SEQUENCE 701 AA; 80169 MW; 15EB43A6FCC08A3 CRC64; </p>	<p> Query Match 71.0%; Score 44; DB 11; Length 701; Best Local Similarity 75.0%; Pred. No. 91; Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0; </p>

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RA Kiewitz C., Eisen J., Timmis K.N., Dueterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida K12440.";
RL Environ. Microbiol. 4:799-808 (2002).
DR EMBL; AE016792; AAN70364.1; -.
DR TIGR; PP4795; -.
DR InterPro; IPR000437; Prok_lipoprot_s.
DR InterPro; IPR007485; RplB.
DR Pfam; PF04330; RplB.1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 201 AA; 22414 MW; BEE46C36E59A65BE CRC64;

Query Match 66.1%; Score 41; DB 16; Length 201;
Best Local Similarity 53.8%; Pred. No. 84;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMORRADQLA 13
:|:|:|:|:|:|
Db 161 QLDELQKADERA 173

RESULT 12
Q9WV62 PRELIMINARY; PRT; 253 AA.
AC Q9WV62;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Kinesin-like protein Kif3A (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Gould R.M., Freund C.M., Hawkins G.A.;
RT "Rat Kinesin probes to use for Northern blot analysis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155925; AAD39242.1; -.
FT NON TER 1
FT NON TER 253
SQ SEQUENCE 253 AA; 30104 MW; 5A61CEC5F5B94B44 CRC64;

Query Match 66.1%; Score 41; DB 11; Length 253;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMORRADQL 12
|||:|:|:|
Db 113 ELEERRKRAEQL 124

RESULT 13
Q9G050 PRELIMINARY; PRT; 315 AA.
AC Q9G050;
DT 01-MAR-2001 (TREMBLrel. 15, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Vp4.
OS Phage phiMH2K.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=145579;
RN [1]
RP SEQUENCE FROM N.A.
RA Fane B.A., Hafenstein S.L., Brentlinger K.L., Burch A.D., Novak C.R.;
RT "The complete genome sequence of the a Microviridae virus, phiMH2K,
RT isolated from Adelovirio bacteriovorus.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF306496; AAG45349.1; -.

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SQ SEQUENCE 315 AA; 37231 MW; EB0BC61D3CF67BFB CRC64;

Query Match 66.1%; Score 41; DB 9; Length 315;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ELEEMORRADQL 12
|||:|:|:|
Db 264 ELAEMQSRKQQL 275

RESULT 14
Q9UYW5 PRELIMINARY; PRT; 480 AA.
AC Q9UYW5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein PYRAB13920.
GN PYRAB13920 OR PAB1455.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GES / Orsay;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248287; CAB50297.1; -.
DR PIR; D75050; D75050.
DR InterPro; IPR007509; DUF515.
DR Pfam; PF04415; DUF515; 1.
DR Hypothetical protein; Complete proteome.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 480 AA; 53536 MW; F10B305BC854B981 CRC64;

Query Match 66.1%; Score 41; DB 17; Length 480;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMORRADQL 12
|||:|:|:|
Db 150 ELEAKKRAEQL 161

RESULT 15
Q9HN61 PRELIMINARY; PRT; 664 AA.
AC Q9HN61;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Vng2238C.
GN VNG2238C.
OC Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng M.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isebnarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).

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DR EMBL; AE005109; AAG20360.1; -.
DR PIR; D84374; D84374.
DR InterPro; IPR001395; Aldo/ket_red.
DR InterPro; IPR007408; DUF460.
DR Pfam; PF04312; DUF460; 1.
DR PROSITE; PS00063; ALDOXETO_REDUCTASE_3; 1.
KW Complete proteome.
SQ SEQUENCE 664 AA; 73964 MW; 708E778DB502269B CRC64;

Query Match 66.1%; Score 41; DB 17; Length 664;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADOL 12
   ||| : |||
Db 494 ELEQRERADEL 505

Search completed: March 4, 2004, 08:29:16
Job time : 50.5789 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 14.3684 Seconds
(without alignments)
47.111 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEEMQRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	62	100.0	206	1 SN25 HUMAN	P13795 homo sapien
2	50	80.6	204	1 SN2A CARAU	P36977 carassius a
3	44	71.0	701	1 KF3A MOUSE	P28741 mus musculus
4	43	69.4	203	1 SN2B CARAU	P36978 carassius a
5	42	67.7	210	1 SN25 TORMA	P36976 torpedo mar
6	41	66.1	157	1 PFDA METKA	Q84797 methanopyru
7	41	66.1	102	1 KF3A HUMAN	Q94436 homo sapien
8	40	64.5	102	1 VAW5 RAT	Q92235 rattus norv
9	40	64.5	1976	1 MYHA BOVIN	Q27991 bos taurus
10	40	64.5	1976	1 MYHA HUMAN	P35580 homo sapien
11	40	64.5	1976	1 MYHA RAT	Q91100 rattus norv
12	40	64.5	2107	1 YLJ2 CAEEL	P34367 caenorhabdi
13	39	62.9	420	1 SYS MYCPN	P75107 mycoplasma
14	39	62.9	1209	1 LBN BOVIN	Q8mi28 bos taurus
15	39	62.9	1220	1 LBN MOUSE	Q8k192 mus musculus
16	39	62.9	1308	1 LBN HUMAN	Q86uk5 homo sapien
17	38	61.3	116	1 VAW5 HUMAN	Q95183 homo sapien
18	38	61.3	349	1 TRUD SALTII	Q82473 salmonella
19	38	61.3	349	1 TRUD SALTII	Q82mf8 salmonella
20	38	61.3	357	1 CADH POPDE	P16577 populus del
21	38	61.3	417	1 YC34 MYCPN	P75537 mycoplasma
22	38	61.3	512	1 VG29 BPMU	Q8t1w5 bacterioph
23	38	61.3	879	1 RASO PYRHO	Q58687 pyrococcus
24	38	61.3	1935	1 MYSS CYPCA	Q90339 cyprinus ca
25	38	61.3	1955	1 PUMA PARUN	Q61308 parascaris
26	37	59.7	460	1 SYS HALMA	P54221 haloarcula
27	37	59.7	466	1 CYPB CAEEL	P52016 caenorhabdi
28	37	59.7	617	1 UVRC THETN	Q8r8n9 thermoanser
29	37	59.7	635	1 DNAK HALMA	Q11100 haloarcula
30	37	59.7	636	1 COS2 CARHY	Q9f8a8 carboxydoth
31	37	59.7	670	1 YDHK ECO57	Q9x638 escherichia
32	37	59.7	670	1 YDHK ECOLI	P76186 escherichia
33	37	59.7	687	1 WRK2 ARATH	Q9fg77 arabidopsis

34	37	59.7	721	1 DNAK APHHA	O52960 aphanothece
35	37	59.7	775	1 CN04 MOUSE	Q8k3x4 mus musculus
36	37	59.7	796	1 CN04 HUMAN	Q9hib7 homo sapien
37	37	59.7	868	1 CLP TRYBB	P31543 trypanosoma
38	37	59.7	1191	1 SMC2 MOUSE	O8c948 mus musculus
39	36	58.1	76	1 KEC2 ECOLI	P13966 escherichia
40	36	58.1	209	1 YNU1 SHIFL	P29770 shigella fl
41	36	58.1	297	1 YUJP HAEIN	P44520 haemophilus
42	36	58.1	338	1 TAP4 HUMAN	Q01664 homo sapien
43	36	58.1	402	1 OPS4 CANAL	P46596 candida alb
44	36	58.1	420	1 NCB2 HUMAN	P80303 homo sapien
45	36	58.1	448	1 VIME CRIGR	P48670 cricetus

ALIGNMENTS

RESULT 1
SN25 HUMAN STANDARD; PRT; 206 AA.
AC P13795; P36974; P70557; P70558; Q81XK3; Q96FM2; Q9BR45;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Synaptoosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).
GN SNAP25 OR SNAP.
OS Homo sapiens (Human),
OS Macaca mulatta (Rhesus macaque),
OS Mus musculus (Mouse),
OS Rattus norvegicus (Rat), and
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606, 9544, 10090, 10116, 9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94156217; PubMed=8112622;
RT "Human cDNA clones encoding two different isoforms of the nerve
terminal protein SNAP-25.";
RL Gene 139:291-292(1994).
RA Bark I.C., Wilson M.C.;
RA "Cloning and sequence analysis of the human SNAP25 cDNA.";
RL Gene 145:313-314(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).
RC SPECIES=Human; TISSUE=Brain;
RX MEDLINE=94333829; PubMed=8056350;
RA Zhao N., Hashida H., Takahashi N., Sakaki Y.;
RA "Cloning and sequence analysis of the human SNAP25 cDNA.";
RL Gene 145:313-314(1994).
RN [3]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC SPECIES=Human; TISSUE=Skeletal muscle;
RX MEDLINE=96332494; PubMed=8760387;
RA Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L.,
RA Gough K.H., Grusovin J., Verkuylen A., Cosgrove L., Alafaci A.,
RA Frenkel M.J., Ward C.W.;
RA "Insulin-responsive tissues contain the core complex protein SNAP-25
(synaptoosomal-associated protein 25) A and B isoforms in addition to
syntaxin 4 and synaptobrevins 1 and 2.";
RL Biochem. J. 317:945-954(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.B., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark I.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leivaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prithalisingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
 RA Swann R.M., Symmore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A.C., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20";
 RL Nature 414:865-871 (2001).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Human; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=M.mullatta; TISSUE=Hippocampus;
 RX Jensen M.J., Smith L.A.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=BALB/c;
 RX MEDLINE=90078337; PubMed=2592413;
 RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
 RA Bloom F.E., Wilson M.C.;
 RT "The identification of a novel synaptosomal-associated protein,
 SNAP-25, differentially expressed by neuronal subpopulations";
 RL J. Cell Biol. 109:3039-3052 (1989).
 RN [8]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=ILS, and ISS;
 RX MEDLINE=21363810; PubMed=11471062;
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
 RT "High-throughput sequence identification of gene coding variants
 within alcohol-related QTLs";
 RL Mamm. Genome 12:657-663 (2001).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tonaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.R., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Taketani Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Vetraro D., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [10]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
 RX Strausberg R.L.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
 RC SPECIES=Cat;
 RX Kataoka M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
 RC SPECIES=Cat; TISSUE=Brain;
 RX Cho A.R., You K.H.;
 RT "Cloning of the SNAP-25 gene from a rat brain cDNA library";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
 RC SPECIES=Cat; TISSUE=Brain;
 RX MEDLINE=99155074; PubMed=10037470;
 RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.;
 RT "SNARE complex proteins, including the cognate pair VAMP-2 and
 syntaxin-4, are expressed in cultured oligodendrocytes";
 RL J. Neurochem. 72:988-998 (1999).
 RN [14]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Chicken; TISSUE=Retina;
 RX MEDLINE=91126080; PubMed=1992470;
 RA Catsicas S., Larhammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
 RA Wilson M.C.;
 RT "Expression of a conserved cell-type-specific protein in nerve
 terminals coincides with synaptogenesis";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789 (1991).
 RN [15]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Chicken;
 RX MEDLINE=93389738; PubMed=8377193;
 RA Bark J.C.;
 RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
 encoding distinct isoforms of the protein";
 RL J. Mol. Biol. 233:67-76 (1993).
 RN [16]
 RP PALMITOYLATION.
 RC SPECIES=Cat;
 RX MEDLINE=93100552; PubMed=1281490;
 RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.;
 RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
 methionine-rich polypeptide in rapid axonal transport and a major

Query Match 100.0%; Score 62; DB 1; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMORRADQLA 13
 |||||
 DB 10 ELEEMORRADQLA 22

RESULT 2

ID SN2A_CARAU STANDARD; PRT; 204 AA.
 AC P36977;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaposomal-associated protein 25A (SNAP-25A).
 GN SNAP-A.
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Carassius.
 OX NCBI_TaxID=7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94068448; PubMed=8248151;
 RA Risinger C., Larhammar D.,
 RT "Multiple loci for synapse protein SNAP-25 in the tetraploid
 goldfish.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
 CC -!- FUNCTION: May play an important role in the synaptic function of
 specific neuronal systems. Associates with proteins involved in
 vesicle docking and membrane fusion.
 CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
 the nerve terminal.
 CC -!- SIMILARITY: Belongs to the SNAP-25 family.
 CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.

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 or send an email to license@isb-sib.ch).

 EMBL; L22973; AAA16337.1; -.
 DR PIR; I50480;
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T-SNARE.
 DR Pfam; PF00835; SNAP-25_1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; t-SNARE; 2.
 DR PROSITE; PS0192; t-SNARE; 2.
 KW Synaposome; Neurone; Repeat; Coiled coil; Multigene family.
 FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
 FT DOMAIN 138 200 T-SNARE COILED-COIL HOMOMOLOGY 2.
 FT DOMAIN 85 92 CYS-RICH.
 SQ SEQUENCE 204 AA; 22843 MW; 458B8ECFCFC09189 CRC64;

Query Match 80.6%; Score 50; DB 1; Length 204;
 Best Local Similarity 76.9%; Pred. No. 0.41;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMORRADQLA 13
 |||:|:|:|:|
 DB 10 ELSDMQRADQLA 22

RESULT 3

KF3A_MOUSE

ID KF3A_MOUSE STANDARD; PRT; 701 AA.
 AC P28741;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin
 motor 3A).
 GN KIF3A OR KIF3
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93077686; PubMed=1447303;
 RA Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M., Hirokawa N.;
 RT "Kinesin family in murine central nervous system.";
 RL J. Cell Biol. 119:1287-1296(1992).
 CC -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR
 MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING
 ACTIVITY IN VITRO.
 CC -!- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ALMOST EXCLUSIVELY IN ADULT BRAIN
 TISSUE (MAINLY IN THE CEREBELLAR GRANULAR LAYER) WITHIN A SINGLE
 TYPE OF NEURONAL CELL.
 CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 II SUBFAMILY.

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 EMBL; D12645; BAA02166.1; -.
 DR PIR; B44259; B44259.
 DR HSSP; P17119; 3KAR.
 DR MGD; MGI:107689; Kif3a.
 DR InterPro; IPR001752; kinesin_motor.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS00067; KINESIN MOTOR DOMAIN2; 1.
 KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
 FT DOMAIN 1 350 KINESIN-MOTOR (BY SIMILARITY).
 FT DOMAIN 351 598 COILED COIL (BY SIMILARITY).
 FT NP BIND 100 107 GLOBULAR.
 FT NP BIND 442 445 ATP (BY SIMILARITY).
 FT DOMAIN 509 512 POLY-GLU.
 FT DOMAIN 509 512 POLY-ARG.
 SQ SEQUENCE 701 AA; 80167 MW; 2405872DF2D85A29 CRC64;

Query Match 71.0%; Score 44; DB 1; Length 701;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMORRADQL 12
 ||||:|:|:|
 DB 505 ELEERRRAEQL 516

RESULT 4

SN2B_CARAU

ID SN2B_CARAU STANDARD; PRT; 203 AA.
 AC P36978;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Synaposomal-associated protein 25B (SNAP-25B).

GN SNAP-B.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=94068448; PubMed=8248151;
RA Risinger C., Larhammar D.;
RA "Multiple loci for synapse protein SNAP-25 in the tetraploid
RT goldfish";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10598-10602(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -!- TISSUE SPECIFICITY: Neurons of the neocortex, hippocampus, and
CC piriform cortex, anterior thalamic nuclei, pontine nuclei, and
CC granule cells of the cerebellum.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; L22976; AAA16538.1; -
CC FIR; I50481; I50481.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS0192; T-SNARE; 2.
CC Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
KW Synaptosome; Neurone; Repeat; Coiled coil; Multigene family.
FT DOMAIN 19 81 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 137 199 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 85 92 CYS-RICH
FT CARBOHYD 77 77 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 203 AA; 22664 MW; 8DFBDEBDE37D6D7 CRC64;

Query Match 69.4%; Score 43; DB 1; Length 203;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
|||:|||||
DB 10 ELTDMQARADQL 21

RESULT 5
SN25_TORMA STANDARD; PRT; 210 AA.
AC P36976;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Synaptosomal-associated protein 25 (SNAP-25).
OS Torpedo marmorata (Marbled electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosqualea; Pristiogaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7788;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Electric lobe;
RX MEDLINE=94043281; PubMed=8226991;
RA Risinger C., Blomqvist A.G., Lundell I., Lambertsson A.,
RA Nassel D., Pieribone V.A., Brodin L., Larhammar D.;
RA "Evolutionary conservation of synaptosome-associated protein 25 kDa
RT (SNAP-25) shown by Drosophila and Torpedo cDNA clones";
RL J. Biol. Chem. 268:24408-24414(1993).
CC -!- FUNCTION: May play an important role in the synaptic function of
CC specific neuronal systems. Associates with proteins involved in
CC vesicle docking and membrane fusion.
CC -!- SUBCELLULAR LOCATION: Complexed with macromolecular elements of
CC the nerve terminal.
CC -!- SIMILARITY: Belongs to the SNAP-25 family.
CC -!- SIMILARITY: Contains 2 t-SNARE coiled-coil homology domains.
CC
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CC
CC EMBL; L22020; AAA49284.1; -
CC FIR; I50552; I50552.
CC InterPro; IPR000928; SNAP-25.
CC InterPro; IPR000727; T-SNARE.
CC Pfam; PF00835; SNAP-25; 1.
CC Pfam; PF05739; SNARE; 1.
CC SMART; SM00397; t-SNARE; 2.
CC PROSITE; PS0192; T-SNARE; 2.
CC Synaptosome; Neurone; Repeat; Coiled coil.
FT DOMAIN 23 85 T-SNARE COILED-COIL HOMOMOLOGY 1.
FT DOMAIN 147 209 T-SNARE COILED-COIL HOMOMOLOGY 2.
FT DOMAIN 88 96 CYS-RICH.
SQ SEQUENCE 210 AA; 23652 MW; 58F2471A9234B8B1 CRC64;

Query Match 67.7%; Score 42; DB 1; Length 210;
Best Local Similarity 75.0%; Pred. No. 7.8;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
|||:|||||
DB 14 EQEEMQRCADQL 25

RESULT 6
PFDA_METKA STANDARD; PRT; 157 AA.
AC Q8TU7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Prefoldin alpha subunit (Gimc alpha subunit).
GN PFDA OR MK1614.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva V.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Nataraj D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
CC -!- FUNCTION: Molecular chaperone capable of stabilizing a range of
CC proteins. Seems to fulfil an ATP-independent, HSP70-like function
CC in archaeal de novo protein folding (By similarity).

CC -!- SUBUNIT: Heterohexamer of two alpha and four beta subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the prefoldin alpha subunit family.
CC
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CC
CC EMBL; AE010451; AM02827.1; -
CC HAMAP; MF 00308; -; 1
CC InterPro; IPR004127; DUF232.
CC Pfam; PF02996; Prefoldin; 1.
CC Chapterone; Complete proteome.
CC KW
CC SEQUENCE 157 AA; 17446 MW; B20BD8ACC978DFA1 CRC64;
CC
CC Query Match 66.1%; Score 41; DB 1; Length 157;
CC Best Local Similarity 61.5%; Pred. No. 8.4;
CC Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 1 ELEMORRADOLA 13
CC ||| ||| :||
CC Db 129 ELQEKQKQAEQLA 141
CC
CC RESULT 7
CC KIF3A HUMAN STANDARD; PRT; 702 AA.
CC ID KIF3A HUMAN
CC AC Q9Y496; Q9Y496; Q9Y6V4;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Kinesin-like protein KIF3A (Microtubule plus end-directed kinesin
CC motor 3A).
CC GN KIF3A OR KIF3.
CC OS Homo sapiens (human).
CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC
CC RX MEDLINE=20018159; PubMed=10548469;
CC RA Whitehead J.L., Wang S.Y., Host-Usinger L., Hoang E., Frazer K.A.,
CC Burnside B.;
CC RT "Photoreceptor localization of the KIF3A and KIF3B subunits of the
CC heterotrimeric microtubule motor kinesin II in vertebrate retina.";
CC RL Exp. Eye Res. 69:491-503(1999).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC
CC RX MEDLINE=22388257; PubMed=12477932;
CC RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
CC RA Brownstein M.J., Usdin T.B., Tohyuki S., Carninci P., Prange C.,
CC RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
CC RA Boeak S.A., McEwan P.J., McKernan K.D., Malek J.A., Gunaratne P.H.,
CC RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CC RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
CC RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
CC RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
CC RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Connolly K.S., Gunning K.M., Davis C.A., Kadner K., Subramanian S.,
RA Miguel T., Lewis K.D., Pridyand J., Alcivar D., Benke J.A.,
RA Bondoc M., Bowen E., Chiang A., Critz P., Jakievic M.A., Lindo K.,
RA Lindquist K., Miller C., Patel S., Piscia C., Riley B.E., Rojeski H.,
RA Samlento R., Yu C., Montenegro M., Aerts A., Chung A., Abrasano A.,
RA Baker M., Gau C., Jett J., Ko C., Beall K., Woolley J.P., Stultz J.L.,
RA Kimmerly W., Martin C.H.;
RL "Sequencing of human chromosome 5.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLATOR FOR
CC MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING
CC ACTIVITY IN VITRO.
CC -!- SUBUNIT: HETERODIMER OF KIF3A AND KIF3B.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC II SUBFAMILY.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC
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CC
CC EMBL; AF041853; AAC72294.1; -
CC EMBL; BC045542; AAH45542.1; -
CC EMBL; AC004237; AAC04475.1; ALT_SEQ.
CC HSSP; P17119; 3KAR.
CC Genew; HGNC:6319; KIF3A.
CC MIM; 604683; -
CC GO; GO:0006996; P:organelle organization and biogenesis; TAS.
CC InterPro; IPR001752; Kinesin_motor.
CC Pfam; PF00225; Kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
CC PROSITE; PS00067; KINESIN_MOTOR_DOMAIN2; 1.
CC KW Motor protein; Microtubule; ATP-binding; Coiled coil; Neurone.
FT DOMAIN 1 350
FT KINESIN-MOTOR.
FT COILED COIL (BY SIMILARITY).
FT DOMAIN 351 599
FT GLOBULAR.
FT NP BIND 100 107
FT ATP (BY SIMILARITY).
FT DOMAIN 443 446
FT POLY-GLU.
FT CONFLICT 151 151
FT E -> G (IN REF. 2).
FT CONFLICT 170 170
FT E -> A (IN REF. 1).
FT CONFLICT 172 172
FT K -> I (IN REF. 2).
SQ SEQUENCE 702 AA; 80385 MW; 88E5D21209BAE14 CRC64;
Query Match 66.1%; Score 41; DB 1; Length 702;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 ELEMORRADQL 12
||| ||| :||
Db 506 ELEERRKAEQL 517
RESULT 8
VAMP5 RAT STANDARD; PRT; 102 AA.
ID VAMP5 RAT
AC Q9Z255;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vesicle-associated membrane protein 5 (VAMP-5) (Myobrevin).
GN

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98395046; PubMed=9725904;
 RA Zeng Q., Subramaniam V.N., Wong S.H., Tang B.L., Parton R.G., Rea S.,
 James D.E., Hong W.;
 RT "A novel synaptobrevin/VAMP homologous protein (VAMP5) is increased
 RT during in vitro myogenesis and present in the plasma membrane.";
 RL Mol. Biol. Cell 9:2423-2437(1998).
 CC -!- FUNCTION: May participate in trafficking events that are
 CC associated with myogenesis, such as myoblast fusion and/or GLUT4
 CC trafficking.
 CC -!- SUBCELLULAR LOCATION: Type IV membrane protein (Probable).
 CC Associated with the plasma membrane as well as intracellular
 CC perinuclear and peripheral vesicular structures of myotubes.
 CC Associated with the trans-Golgi, but not with the cis-Golgi
 CC apparatus (By similarity).
 CC -!- INDUCTION: During myogenesis.
 CC -!- SIMILARITY: Belongs to the synaptobrevin family.
 CC -!- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.
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 CC
 DR EMBL: AF054826; AAC97474.1; -;
 DR InterPro: IPR001388; Synaptobrevin.
 DR Pfam: PF00957; synaptobrevin; 1.
 DR PRINTS: PR00219; SYNAPTOBREVIN.
 DR ProDom: PD001229; Synaptobrevin; 1.
 DR PROSITE: PS00417; SYNAPTOBREVIN; FALSE_NEG.
 DR PROSITE: PS00892; V-SNARE; 1.
 KW Myogenesis; Transmembrane; Coiled coil; Multigene family.
 FT DOMAIN 1 72 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 73 93 ANCHOR FOR TYPE IV MEMBRANE PROTEIN
 FT DOMAIN 94 102 VESICULAR (POTENTIAL).
 FT DOMAIN 5 65 V-SNARE COILED-COIL HOMOLGY.
 FT SEQUENCE 102 AA; 11495 MW; 6AC37413597236BC CRC64;
 SQ
 Query Match 64.5%; Score 40; DB 1; Length 102;
 Best Local Similarity 66.7%; Pred. No. 7.9;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMORRADQL 12
 DB 5 ELERCQADQV 16
 RESULT 9
 MYHA BOVIN STANDARD; PRT; 1976 AA.
 AC Q27991;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
 DE type B) (Nonmuscle myosin heavy chain-B) (NMMEC-B).
 GN MYH10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ohara M., Ishiguro N., Shinagawa M.;
 RT "Bos taurus nonmuscle myosin heavy chain B mRNA, complete cds.";
 RN Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE OF 204-302 FROM N.A.
 RX MEDLINE=95301542; PubMed=7782316;
 RA Itoh K., Adelstein R.S.;
 RT "Neuronal cell expression of inserted isoforms of vertebrate nonmuscle
 RT myosin heavy chain II-B.";
 RL J. Biol. Chem. 270:14533-14540(1995).
 CC -!- FUNCTION: Cellular myosin appears to play a role in cytokinesis,
 CC cell shape, and specialized functions such as secretion and
 CC capping (By similarity).
 CC -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy
 CC chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2
 CC regulatory light chain subunits (MLC-2).
 CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
 CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
 CC characteristic for alpha-helical coiled coils.
 CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -!- SIMILARITY: Contains 1 IQ domain.
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 CC
 DR EMBL: AB022023; BAA36494.1; -;
 DR EMBL: U15716; AAA87715.1; -;
 DR HSP: P10587; IBR2.
 DR InterPro: IPR000048; IQ region.
 DR PRINTS: PR001609; myosin head.
 DR ProDom: IPR004009; Myosin N.
 DR InterPro: IPR002928; Myosin tail.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF00612; IQ; 1.
 DR Pfam: PF00063; myosin head; 1.
 DR Pfam: PF02736; Myosin N; 1.
 DR Pfam: PF01576; Myosin tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR MYOSIN; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
 KW Multigene family.
 FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
 FT DOMAIN 786 815 IQ.
 FT DOMAIN 845 1976 COILED COIL (POTENTIAL).
 FT NP BIND 178 185 ATP (POTENTIAL).
 SQ SEQUENCE 1976 AA; 229097 MW; 6144354451C0F790 CRC64;
 Query Match 64.5%; Score 40; DB 1; Length 1976;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ELEMORRADQL 12
 DB 874 ELEEMERKHQQL 885
 RESULT 10
 MYHA HUMAN STANDARD; PRT; 1976 AA.
 AC P35580;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
 DE type B) (Nonmuscle myosin heavy chain-B) (NMMEC-B).
 GN MYH10.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

DE type B) (Nonmuscle myosin heavy chain-B) (NMHC-B).
GN MYH10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96025307; PubMed=7499478;
RA Phillips C.L., Yamakawa K., Adelstein R.S.;
RT "Cloning of the cDNA encoding human nonmuscle myosin heavy chain-B and
RT analysis of human tissues with isoform-specific antibodies.";
RL J. Muscle Res. Cell Motil. 16:379-389(1995).
RN [2]
RP SEQUENCE OF 63-722 FROM N.A.
RX MEDLINE=91316803; PubMed=1860190;
RA Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa K.,
RA Gdula D., Adelstein R.S., Weir L.;
RT "Human nonmuscle myosin heavy chains are encoded by two genes located
RT on different chromosomes.";
RL Circ. Res. 69:530-539(1991).
CC -!- FUNCTION: Cellular myosin appears to play a role in cytokinesis,
CC cell shape, and specialized functions such as secretion and
CC capping.
CC -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy
CC chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2
CC regulatory light chain subunits (MLC-2).
CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC
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CC
CC EMBL; M69181; AAA99177.1; -.
DR PIR; A59252; A59252.
DR HSSP; P10587; IBR2.
DR GENE; HGNC:7568; MYH10.
DR MIM; 160776; -.
DR GO; GO:0016459; C:myosin; NAS.
DR GO; GO:0003779; F:actin binding; NAS.
DR GO; GO:0005524; F:ATP binding; NAS.
DR GO; GO:0000910; P:cytokinesis; NAS.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
KW Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
KW Multigene family.
FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
FT DOMAIN 786 815 IQ.
FT DOMAIN 845 1976 COILED COIL (POTENTIAL).
FT NP_BIND 178 185 ATP (POTENTIAL).
SQ SEQUENCE 1976 AA; 228938 MW; B2BB87FF35E124F CRC64;
Query Match 64.5%; Score 40; DB 1; Length 1976;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ELEEMQRRADQL 12
|||||: ||
DB 874 ELEEMERKHOQL 885
RESULT 11
MYHA RAT
ID MYHA RAT STANDARD; PRT; 1976 AA.
AC Q9UL70;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
DE type B) (Nonmuscle myosin heavy chain-B) (NMHC-B).
GN MYH10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=20483650; PubMed=11027611;
RA Yam J.W.P., Chan K.W., Li N., Hsiao W.L.W.;
RT "Molecular cloning and functional analysis of the promoter region of
RT rat nonmuscle myosin heavy chain-B gene.";
RL Biochem. Biophys. Res. Commun. 276:1203-1209(2000).
CC -!- FUNCTION: Cellular myosin appears to play a role in cytokinesis,
CC cell shape, and specialized functions such as secretion and
CC capping.
CC -!- SUBUNIT: Myosin is a hexameric protein that consists of 2 heavy
CC chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2
CC regulatory light chain subunits (MLC-2).
CC -!- DOMAIN: The rodlike tail sequence is highly repetitive, showing
CC cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
CC characteristic for alpha-helical coiled coils.
CC -!- SIMILARITY: Contains 1 myosin-like globular head domain.
CC -!- SIMILARITY: Contains 1 IQ domain.
CC
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CC
CC EMBL; AF139055; AAF61445.1; -.
DR HSSP; P10587; IBR2.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR001609; myosin_head.
DR InterPro; IPR004009; Myosin_N.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
KW Myosin; ATP-binding; Calmodulin-binding; Actin-binding; Coiled coil;
KW Multigene family.
FT DOMAIN 1 785 MYOSIN HEAD-LIKE.
FT DOMAIN 786 815 IQ.
FT DOMAIN 845 1976 COILED COIL (POTENTIAL).
FT NP_BIND 178 185 ATP (POTENTIAL).
SQ SEQUENCE 1976 AA; 228963 MW; E32708BF9BF2B470 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 1976;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
 |||||:|:
 Db 874 ELEMORRADQL 885

RESULT 12
 YLJ2 CAEL STANDARD; PRT; 2107 AA.
 AC P34367; 018736;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Hypothetical protein C50C3.2 in chromosome III.
 GN C50C3.2/C50C3.3.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kersey J., Kirsten J., Laisner N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden K.,
 RA Sultston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38 (1994).

RN [2]
 RP REVISIONS.
 RA Waterston R.;
 RC Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

RL -1- SIMILARITY: Belongs to the spectrin family.
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CC EMBL; L14433; AAA27974.2;
 CC WormPep; C50C3.2; CE01861.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR002017; Spectrin.
 DR Pfam; PF00036; ehand; 2.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EPH; 2.
 DR SMART; SM00150; SPC; 6.
 DR PROSITE; PS00018; EF_HAND; 1.
 KW Hypothetical protein; Calcium-binding; Repeat.
 FT CA BIND 2025 2036 EF-HAND (POTENTIAL).
 SQ SEQUENCE 2107 AA; 246123 MW; B5C3C51EC0EDA2E9 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 2107;
 Best Local Similarity 53.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 13
 |||||:|:
 Db 1272 DIERMQKHDELA 1284

RESULT 13
 SYS_MYCPN STANDARD; PRT; 420 AA.
 AC P75107;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Seryl-tRNA synthetase (EC 6.1.1.11) (Serrine-tRNA ligase) (SERRS).
 GN SERS OR MEN005 OR MP149.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelsreich R., Hilbert H., Piagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449 (1996).
 CC -1- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
 CC + L-seryl-tRNA(Ser).
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.

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CC EMBL; AE000016; AAB95797.1;
 DR PIR; S73475; S73475.
 DR HSP; P34945; 1SER.
 DR HAMAP; MF 00176; -1.
 DR InterPro; IPR002314; tRNA-synt 2b.
 DR InterPro; IPR002317; tRNA-synt_ser.
 DR InterPro; IPR006195; tRNA_ligase_II.
 DR Pfam; PF02403; Seryl-tRNA N; 1.
 DR Pfam; PF00587; tRNA-synt 2b; 1.
 DR PRINTS; PR00981; TRNASYNTHSER.
 DR TIGRFAMs; TIGR00414; sers; 1.
 DR PROSITE; PS50862; AA TRNA LIGASE II; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 420 AA; 47924 MW; 9BC071823D20998E CRC64;

Query Match 62.9%; Score 39; DB 1; Length 420;
 Best Local Similarity 66.7%; Pred. No. 46;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
 |||||:|:
 Db 292 ELEMORRADQL 303

RESULT 14
 LEN BOVIN STANDARD; PRT; 1209 AA.
 AC Q8M128;
 DT 15-MAR-2004 (Rel. 43, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Limbin.

GN EVC2 OR LEN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE FROM N.A., AND DISEASE.
RP SEQUENCE=bone;
RC TISSUE=bone;
RX MEDLINE=22155879; PubMed=12136126;
RA Takeda H., Takami M., Oguni T., Tsuji T., Yoneda K., Sato H.,
RA Ihara N., Itoh T., Kata S.R., Mishina Y., Momack J.E., Moritomo Y.,
RA Sugimoto Y., Kunieda T.;
RA "Positional cloning of the gene LIMBIN responsible for bovine
RT chondrodysplastic dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10549-10554(2002).
CC -!- FUNCTION: Plays a critical role in bone formation and skeletal
CC development.
CC -!- DISEASE: Defects in EVC2 are the cause of bovine chondrodysplastic
CC dwarfism (BCD). BCD is an autosomal recessive disorder
CC characterized by short limbs, joint abnormalities and ateliosis.
CC -----
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CC -----
CC EMBL; AB083065; BAC06588.1; -;
KW Transmembrane; Coiled coil; Dwarfism.
FT TRANSMEM 201 221 POTENTIAL.
FT DOMAIN 355 394 COILED COIL (POTENTIAL).
FT DOMAIN 553 697 COILED COIL (POTENTIAL).
FT DOMAIN 920 1012 COILED COIL (POTENTIAL).
SQ SEQUENCE 1209 AA; 137811 MW; D78106F1001785AB CRC64;
Query Match 62.9%; Score 39; DB 1; Length 1209;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY |||||
Db 621 LEELQRLQQA 632
RESULT 15
LEN MOUSE
ID LEN MOUSE STANDARD; PRT; 1220 AA.
AC O8KIG2; O8BRF3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Limbin.
GN EVC2 OR LEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=limb bud;
RX MEDLINE=22155879; PubMed=12136126;
RA Takeda H., Takami M., Oguni T., Tsuji T., Yoneda K., Sato H.,
RA Ihara N., Itoh T., Kata S.R., Mishina Y., Momack J.E., Moritomo Y.,
RA Sugimoto Y., Kunieda T.;
RA "Positional cloning of the gene limbin responsible for bovine
RT chondrodysplastic dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10549-10554(2002).
CC [2]
RN SEQUENCE FROM N.A.
RP STRAIN=FVB/N; TISSUE=Kidney;
DR EMBL; AB083066; BAC06589.1; -;
DR EMBL; BC037473; AAH37473.1; -;

RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [3]
RP SEQUENCE OF 21-744 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nixakdo I., Oeato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schraml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gassterland I., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Plays a critical role in bone formation and skeletal
CC development. May be involved in early embryonic morphogenesis.
CC -!- TISSUE SPECIFICITY: Expressed in long and cranial bones, kidney
CC and heart. Strongly expressed in proliferating chondrocytes,
CC osteoblasts and osteoclasts.
CC -!- DEVELOPMENTAL STAGE: Found in the embryo at day E7, E11, E15, and
CC E17. At the limb bud formation stage E11, it is expressed in fore-
CC and hindlimb buds, branchial arches, and facial primordia.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB083066; BAC06589.1; -;
DR EMBL; BC037473; AAH37473.1; -;

```

DR EMBL; AK044977; BAC32167.1; ALT_INIT.
DR MGD; MGI:1915775; Evc2.
KW Transmembrane; Coiled coil.
FT TRANSMEM 211 231 POTENTIAL.
FT DOMAIN 355 404 COILED COIL (POTENTIAL).
FT DOMAIN 563 644 COILED COIL (POTENTIAL).
FT DOMAIN 854 875 COILED COIL (POTENTIAL).
FT DOMAIN 920 1005 COILED COIL (POTENTIAL).
SQ SEQUENCE 1220 AA; 137638 MW; E67671714A866B1D CRC64;

Query Match      62.9%; Score 39; DB 1; Length 1220;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Cy      2 LEEMQRADQLA 13
      |||:|
Db      631 LEEIQERLDQAA 642

Search completed: March 4, 2004, 08:25:56
Job time : 15.3684 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 17.7895 Seconds
(without alignments) 70.294 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEEMORRADOLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	100.0	206	2 A37861	synaptosomal-assoc
2	62	100.0	206	2 153735	nerve terminal pro
3	62	100.0	206	2 167823	nerve terminal pro
4	62	100.0	206	2 A33623	synaptosomal-assoc
5	62	100.0	249	2 S38308	SNAP-25 protein -
6	62	100.0	249	2 S38309	SNAP-25 protein -
7	57	91.9	56	2 S36812	probable synapse-a
8	50	80.6	204	2 150480	synapse protein SN
9	44	71.0	701	1 B44259	kinesin-related pr
10	43	69.4	203	2 150481	synapse protein SN
11	42	67.7	210	2 150552	synapse protein -
12	41	66.1	480	2 D75050	hypothetical prote
13	41	66.1	664	2 D84374	hypothetical prote
14	40	64.5	149	2 AB1645	Protein gp28 (Bact
15	40	64.5	924	2 S06117	myosin heavy chain
16	40	64.5	1009	2 S44621	C50C3.2 protein -
17	40	64.5	1976	2 A59252	myosin heavy chain
18	40	64.5	1999	1 S21801	myosin heavy chain
19	40	64.5	2007	1 B43402	myosin heavy chain
20	39	62.9	119	2 E98090	hypothetical prote
21	39	62.9	190	2 G82840	hypothetical prote
22	39	62.9	420	2 S73475	serine-tRNA ligase
23	39	62.9	532	2 G87912	protein B0205.9 [i
24	38	61.3	91	2 B75601	hypothetical prote
25	38	61.3	136	2 D70361	transcription regu
26	38	61.3	266	2 A12283	hypothetical prote
27	38	61.3	294	2 S75135	hypothetical prote
28	38	61.3	341	2 S31571	cinnamyl-alcohol d
29	38	61.3	349	2 AC0856	conserved hypothet

30 38 61.3 357 2 T09141
31 38 61.3 417 2 S73923
32 38 61.3 500 2 A82497
33 38 61.3 702 2 T16401
34 38 61.3 879 2 C71083
35 38 61.3 920 2 AD2143
36 38 61.3 1210 2 H88451
37 38 61.3 1955 2 T30934
38 37 59.7 283 2 S42393
39 37 59.7 309 2 B92000
40 37 59.7 460 2 T47108
41 37 59.7 466 2 T18575
42 37 59.7 470 2 AC0049
43 37 59.7 474 2 F87152
44 37 59.7 506 2 AH0509
45 37 59.7 609 2 T28896

ALIGNMENTS

RESULT 1

A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:CatScas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coincid
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELEEMORRADOLA 13
Db 10 ELEEMORRADOLA 22

RESULT 2

153735
nerve terminal protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: 153735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:L19760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELEEMORRADOLA 13
Db 10 ELEEMORRADOLA 22

```
RESULT 3
I67823
nerv terminal protein - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:I19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 4
A33623
synaptosomal-associated 25K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differ
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M2012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

Query Match 100.0%; Score 62; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 5
S38308
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38308
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38308
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 6
S38309
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 7
S36812
probable synapse-associated 28K protein - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C:Accession: S36812
R:Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 235-240, 1993
A:Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A:Reference number: S36811; MUID:93374072; PMID:8365494
A:Accession: S36812
A:Molecule type: protein
A:Residues: 1-56 <HOR>
A:Experimental source: brain

Query Match 91.9%; Score 57; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEMORRADOLA 13
|||||
DB 1 LEEMORRADOLA 12

RESULT 8
I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DBJ
```

```
Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 6
S38309
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 62; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
DB 10 ELEMORRADOLA 22

RESULT 7
S36812
probable synapse-associated 28K protein - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C:Accession: S36812
R:Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 235-240, 1993
A:Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A:Reference number: S36811; MUID:93374072; PMID:8365494
A:Accession: S36812
A:Molecule type: protein
A:Residues: 1-56 <HOR>
A:Experimental source: brain

Query Match 91.9%; Score 57; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEEMORRADOLA 13
|||||
DB 1 LEEMORRADOLA 12

RESULT 8
I50480
synapse protein SNAP-25 - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50480
R:Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A:Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A:Reference number: A49632; MUID:94068448; PMID:8248151
A:Accession: I50480
A:Status: preliminary; translated from GB/EMBL/DBJ
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A;Molecule type: mRNA
A;Residues: 1-204 <RIS>
A;Cross-references: GB:I22973; NID:G349426; PIDN:AAA16537.1; PID:G349427
C;Genetics:
A;Gene: SNAP-25

Query Match 80.6%; Score 50; DB 2; Length 204;
Best Local Similarity 76.9%; Pred. No. 0.73; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1

QY 1 ELEMORRADQLA 13
|||:|||||
Db 10 ELSDMQRADQLA 22
|||:|||||

RESULT 9
B44259
kinesin-related protein KIF3A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C;Accession: B44259; S27872
R;Alizawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:1447303
A;Accession: B44259
A;Molecule type: mRNA
A;Residues: 1-701 <ALZ>
A;Cross-references: EMBL:D12645; NID:G220469; PIDN:BAA02166.1; PID:G220470
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118911)
C;Complex: heterodimer with KIF3B (PIR:A57107); the KIF3A/3B heterodimer associates with
C;Function:
A;Description: KIF3 complex is a motor protein that provides anterograde fast axonal tra
C;Superfamily: kinesin-related protein KIF3; kinesin motor domain homology
C;Keywords: ATP; coiled coil; heterodimer; heterotrimer; microtubule binding; nucleotide
F;1-368/Domain: head globular #status predicted <HGL>
F;15-351/Domain: kinesin motor domain homology <KMOT>
F;100-107/Region: nucleotide-binding motif A (p-loop)
F;369-599/Domain: helical rod #status predicted <ROD>
F;600-701/Domain: tail globular #status predicted <TGL>
F;106/Binding site: ATP (lys) #status predicted

Query Match 71.0%; Score 44; DB 1; Length 701;
Best Local Similarity 75.0%; Pred. No. 23; Indels 1; Gaps 0;
Matches 9; Conservative 2; Mismatches 1

QY 1 ELEMORRADQL 12
|||:|||||
Db 505 ELEERRRAEQL 516
|||:|||||

RESULT 10
I50481
synapse protein SNAP-25 - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50481
R;Risinger, C.; Larhammar, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993
A;Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.
A;Reference number: A49632; MUID:94068448; PMID:8248151
A;Accession: I50481
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-203 <RIS>
A;Cross-references: GB:I22976; NID:G349430; PIDN:AAA16538.1; PID:G349431
C;Genetics:
A;Gene: SNAP-25

Query Match 69.4%; Score 43; DB 2; Length 203;
Best Local Similarity 75.0%; Pred. No. 9.6; Indels 2; Gaps 0;
Matches 9; Conservative 1; Mismatches 2

QY 1 ELEMORRADQL 12
|||:|||||
Db 10 ELTDQARADQL 21
|||:|||||

RESULT 11
I50552
synapse protein - marbled electric ray
C;Species: Torpedo marmorata (marbled electric ray)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50552
R;Risinger, C.; Blomqvist, A.G.; Lundell, I.; Lambertson, A.; Nassel, D.; Pieribone, V.
J. Biol. Chem. 268, 24408-24414, 1993
A;Title: Evolutionary conservation of synaptosome-associated protein 25 kDa (SNAP-25) sh
A;Reference number: A49513; MUID:94043281; PMID:8226991
A;Accession: I50552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-210 <RIS>
A;Cross-references: GB:L22020; NID:G431296; PIDN:AAA49284.1; PID:G431297

Query Match 67.7%; Score 42; DB 2; Length 210;
Best Local Similarity 75.0%; Pred. No. 14; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 2

QY 1 ELEMORRADQL 12
|||:|||||
Db 14 EOEENQCADQI 25
|||:|||||

RESULT 12
D75050
Hypothetical protein PAB1455 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
C;Accession: D75050
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A;Reference number: A75001
A;Accession: D75050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB50297.1; PID:G545881
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1455
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1455

Query Match 66.1%; Score 41; DB 2; Length 480;
Best Local Similarity 66.7%; Pred. No. 47; Indels 1; Gaps 0;
Matches 8; Conservative 3; Mismatches 1

QY 1 ELEMORRADQL 12
|||:|||||
Db 150 ELEAKRRABEL 161
|||:|||||

RESULT 13
DB4374
Hypothetical protein Vng2238c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: DB4374
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable
; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: D84374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-664 <STO>
A;Cross-references: GB:AE004437; NID:g10581651; PIDN:AAG20360.1; GSPDB:GNC00138
C;Genetics:
A;Gene: VNG2238C

Query Match 66.1%; Score 41; DB 2; Length 664;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELEMQRADQL 12
||||: |||
Db 494 ELEQRADQL 505

RESULT 14

AB1645
Protein gp28 (Bacteriophage A118) [imported] - Listeria innocua (strain Clp11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB1645
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
-; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Me
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1645
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96930.1; PID:g16414186; GSPDB:GNC00178
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: lin1699

Query Match 64.5%; Score 40; DB 2; Length 149;
Best Local Similarity 53.8%; Pred. No. 21;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELEMQRADQLA 13
||||: |||
Db 64 ELEDLEKNADDLA 76

RESULT 15

S06117
myosin heavy chain, nonmuscle (clone lambda-FMHC) - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Jun-2000
C;Accession: S06117
R;Katsumagawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
A;Title: Two distinct nonmuscle myosin-heavy-chain mRNAs are differentially expressed in
s.
A;Reference number: S06116; MUID:90032648; PMID:2806244
A;Accession: S06117
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-924 <KAT>
A;Cross-references: GB:X17590
A;Note: this translation is not annotated in GenBank entry GGMHCFC, release 114
C;Superfamily: myosin heavy chain; myosin motor domain homology
F:1-303/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 64.5%; Score 40; DB 2; Length 924;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ELEMQRADQL 12
||||: |||
Db 406 ELEMERKHOOL 417

Search completed: March 4, 2004, 08:29:54
JOB time : 18.7895 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:20 ; Search time 37.6316 Seconds
(without alignments)
72.944 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEMORRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/ECT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	206	10 US-09-942-024-2	Sequence 2, Appli
2	62	100.0	206	10 US-09-942-024-7	Sequence 7, Appli
3	62	100.0	206	10 US-09-942-024-12	Sequence 12, Appl
4	62	100.0	206	10 US-09-942-098-2	Sequence 2, Appli
5	62	100.0	206	10 US-09-942-098-7	Sequence 7, Appli
6	62	100.0	206	10 US-09-942-098-12	Sequence 12, Appl
7	62	100.0	249	10 US-09-942-024-16	Sequence 16, Appl
8	62	100.0	249	10 US-09-942-098-16	Sequence 16, Appl
9	43	69.4	203	10 US-09-942-024-14	Sequence 14, Appl
10	43	69.4	203	10 US-09-942-098-14	Sequence 14, Appl
11	40	64.5	312	10 US-09-976-782-32	Sequence 32, Appl
12	40	64.5	312	15 US-10-080-334-167	Sequence 167, App
13	40	64.5	312	15 US-10-080-334-188	Sequence 188, App
14	40	64.5	312	15 US-10-080-334-270	Sequence 270, App
15	40	64.5	312	15 US-10-231-913-260	Sequence 260, App

16	40	64.5	1009	15	US-10-369-493-5795	Sequence 5795, Ap
17	40	64.5	1999	15	US-10-028-248A-107	Sequence 107, App
18	40	64.5	1999	15	US-10-107-782-107	Sequence 107, App
19	39	62.9	442	14	US-10-241-220-110	Sequence 110, App
20	38	61.3	102	9	US-09-745-763-6	Sequence 6, Appli
21	38	61.3	116	14	US-10-308-279-68	Sequence 68, Appl
22	38	61.3	116	14	US-10-357-028-4	Sequence 4, Appli
23	38	61.3	116	15	US-10-264-237-1808	Sequence 1808, Ap
24	38	61.3	173	9	US-09-272-809-16	Sequence 16, Appl
25	38	61.3	357	9	US-09-947-027-9	Sequence 9, Appli
26	38	61.3	357	13	US-10-091-009-9	Sequence 9, Appli
27	38	61.3	870	14	US-10-156-761-12048	Sequence 12048, A
28	38	61.3	879	15	US-10-369-493-1271	Sequence 1271, Ap
29	38	61.3	879	15	US-10-369-493-20337	Sequence 20337, A
30	37	59.7	70	14	US-10-078-090-161	Sequence 161, App
31	37	59.7	229	15	US-10-374-780A-1453	Sequence 1453, Ap
32	37	59.7	324	15	US-10-369-493-8329	Sequence 8329, Ap
33	37	59.7	687	10	US-09-934-455-18	Sequence 18, Appl
34	37	59.7	687	14	US-10-295-403-76	Sequence 76, Appl
35	37	59.7	687	15	US-10-374-780A-174	Sequence 174, App
36	37	59.7	723	13	US-10-044-205A-32	Sequence 32, Appl
37	37	59.7	796	13	US-10-044-205A-31	Sequence 31, Appl
38	37	59.7	851	14	US-10-156-761-9933	Sequence 9333, Ap
39	36	58.1	21	14	US-10-113-424-96	Sequence 96, Appl
40	36	58.1	25	14	US-10-360-053-27	Sequence 27, Appl
41	36	58.1	57	9	US-09-864-761-41864	Sequence 41864, A
42	36	58.1	176	15	US-10-264-049-4068	Sequence 4068, Ap
43	36	58.1	244	15	US-10-369-493-2951	Sequence 2951, Ap
44	36	58.1	256	15	US-10-369-493-19362	Sequence 19362, A
45	36	58.1	295	15	US-10-369-493-18283	Sequence 18283, A

ALIGNMENTS

RESULT 1
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-Ar 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELEMORRADQLA 13
|||
Db 10 ELEMORRADQLA 22

RESULT 2
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
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Db 10 ELEMORRADOLA 22

RESULT 3
US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
Db 10 ELEMORRADOLA 22

RESULT 4
US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELEMORRADOLA 13
|||||
Db 10 ELEMORRADOLA 22
RESULT 5
US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
Db 10 ELEMORRADOLA 22

RESULT 6
US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match 100.0%; Score 62; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
|||||
Db 10 ELEMORRADOLA 22

RESULT 7
US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1

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; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-024-16

Query Match      100.0%; Score 62; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQIA 13
   |||||
Db 10 ELEMORRADQIA 22

RESULT 8
US-09-942-098-16
; Sequence 16, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-942-098-16

Query Match      100.0%; Score 62; DB 10; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADQIA 13
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Db 10 ELEMORRADQIA 22

RESULT 9
US-09-942-024-14
; Sequence 14, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-024-14

Query Match      69.4%; Score 43; DB 10; Length 203;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
   |||||
Db 10 ELEMORRADQL 21

RESULT 10
US-09-942-098-14
; Sequence 14, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Carassius auratus
US-09-942-098-14

Query Match      69.4%; Score 43; DB 10; Length 203;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMORRADQL 12
   |||||
Db 10 ELEMORRADQL 21

RESULT 11
US-09-976-782-32
; Sequence 32, Application US/09976782
; Publication No. US20030190715A1
; GENERAL INFORMATION:
; APPLICANT: Grosse et al
; TITLE OF INVENTION: No. US20030190715a1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-157
; CURRENT APPLICATION NUMBER: US/09/976,782
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,113
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,662
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,732
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,625
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,703
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/241,190
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,637
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/240,669
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,455
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/240,648
; PRIOR FILING DATE: 2000-10-16
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; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 32
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Consensus
; OTHER INFORMATION: sequence
US-09-976-782-32

Query Match 64.5%; Score 40; DB 10; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMQRADQL 12
|:|:|:|:|
DB 55 EIEELRRQIDQL 66

RESULT 12

US-10-080-334-167
; Sequence 167, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526

; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 167
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-167

Query Match 64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEEMQRADQL 12
|:|:|:|:|
DB 55 EIEELRRQIDQL 66

RESULT 13

US-10-080-334-188
; Sequence 188, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677


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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/319,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 188
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-188

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Query Match      64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ELEMORRADQL 12
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Db      55 EIEELRRQIDQL 66

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RESULT 14

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US-10-080-334-270
; Sequence 270, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980

```

```

; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 270
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-270

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Query Match      64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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QY      1 ELEMORRADQL 12
        |:|:|:|:|:|
Db      55 EIEELRRQIDQL 66

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RESULT 15

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US-10-231-913-260
; Sequence 260, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eisen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same

```

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; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 260
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-260

Query Match      64.5%; Score 40; DB 15; Length 312;
Best Local Similarity 58.3%; Pred. No. 75;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ELEMORRADQL 12
      |::|::|
Db      55 EIELRRQIDQL 66

Search completed: March 4, 2004, 08:30:59
Job time : 37.8316 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	Count				
1	62	100.0	68	4	US-09-621-976-7614	Sequence 7614, Appl	
2	62	100.0	206	1	US-08-393-985-18	Sequence 18, Appl	
3	62	100.0	206	3	US-08-819-286-1	Sequence 1, Appl	
4	40	84.5	415	4	US-09-252-991A-30511	Sequence 30511, A	
5	38	61.3	116	3	US-08-621-018B-4	Sequence 4, Appl	
6	38	61.3	116	4	US-09-483-465-4	Sequence 4, Appl	
7	38	61.3	509	4	US-09-252-991A-23182	Sequence 23182, A	
8	38	61.3	639	2	US-08-557-309B-37	Sequence 37, Appl	
9	38	61.3	639	3	US-08-834-306-37	Sequence 37, Appl	
10	38	61.3	639	3	US-08-993-674A-37	Sequence 37, Appl	
11	38	61.3	639	4	US-09-256-976-37	Sequence 37, Appl	
12	38	61.3	931	4	US-09-252-991A-22550	Sequence 22550, A	
13	37	59.7	513	4	US-09-489-039A-13840	Sequence 13840, A	
14	36	58.1	21	4	US-09-223-007A-96	Sequence 96, Appl	
15	36	58.1	171	4	US-09-252-991A-24357	Sequence 24357, A	
16	36	58.1	418	4	US-09-489-039A-10840	Sequence 10840, A	
17	36	58.1	466	4	US-09-610-401-3	Sequence 3, Appl	
18	36	58.1	466	4	US-09-610-401-4	Sequence 4, Appl	
19	36	58.1	466	4	US-09-167-206-12	Sequence 12, Appl	
20	36	58.1	514	4	US-09-107-532A-6282	Sequence 6282, Appl	
21	36	58.1	567	4	US-09-489-039A-10840	Sequence 10840, A	
22	36	58.1	823	4	US-09-252-991A-21027	Sequence 21027, A	
23	36	58.1	1441	4	US-09-252-991A-28143	Sequence 28143, A	
24	35	56.5	29	4	US-08-894-139-14	Sequence 14, Appl	
25	35	56.5	102	3	US-09-383-586-34	Sequence 34, Appl	
26	35	56.5	112	3	US-08-857-076-75	Sequence 75, Appl	
27	35	56.5	147	3	US-09-383-586-35	Sequence 35, Appl	

QY 1 ELEEMORRADOLA 13
 Db 10 ELEEMORRADOLA 22

RESULT 2
 US-08-393-985-18
 : Sequence 18, Application US/08393985
 : Patent No. 5693476
 : GENERAL INFORMATION:
 : APPLICANT: Scheller, Richard H.
 : TITLE OF INVENTION: Methods and Compositions for Modulation
 : TITLE OF INVENTION: of Vesicular Release
 : NUMBER OF SEQUENCES: 35
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dehlinger & Associates
 : STREET: 350 Cambridge Avenue, Suite 250
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94306
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0. Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match      100.0%; Score 62; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELEEMQRRADQLA 13
Db      10 ELEEMQRRADQLA 22

RESULT 4
US-09-252-991A-30511
; Sequence 30511, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30511
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30511

Query Match      64.5%; Score 40; DB 4; Length 415;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 LEEMQRRADQLA 13
Db      65 VEEQQRVVDHLA 76

RESULT 5
US-08-621-018B-4
; Sequence 4, Application US/08621018B
; Patent No. 6060239
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Murry, Lynn B.
; TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,018B
; FILING DATE: March 22, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0029-1 CIP
; TELECOMMUNICATION INFORMATION:

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match      100.0%; Score 62; DB 3; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ELEEMQRRADQLA 13
Db      10 ELEEMQRRADQLA 22

RESULT 3
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montcal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1
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TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: LUNGN0T01
 CLONE: 122826
 US-08-621-018B-4

Query Match 61.3%; Score 38; DB 3; Length 116;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
 :||:|:|:
 Db 33 KLAELQQRSDQL 44

RESULT 6

US-09-483-665-4
 Sequence 4, Application US/09483665
 Patent No. 6534275

GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.
 APPLICANT: Hawkins, Phillip R.
 APPLICANT: Seilhamer, Jeffrey J.
 APPLICANT: Murry, Lynn E.
 TITLE OF INVENTION: CELLUBREVIN HOMOLOGS
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/483,665
 FILING DATE: Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/621,018
 FILING DATE: March 22, 1996
 APPLICATION NUMBER: 08/409,373
 FILING DATE: March 23, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Hamlet-Cox, Diana
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-849-8886

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 116 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 IMMEDIATE SOURCE:
 LIBRARY: LUNGN0T01
 CLONE: 122826
 US-09-483-665-4

Query Match 61.3%; Score 38; DB 4; Length 116;
 Best Local Similarity 58.3%; Pred. No. 43;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
 :||:|:|:
 Db 33 KLAELQQRSDQL 44

RESULT 7

US-09-252-991A-23182
 Sequence 23182, Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 23182
 LENGTH: 509
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-23182

Query Match 61.3%; Score 38; DB 4; Length 509;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ELEMQRADQL 12
 :||:|:|:
 Db 349 ELECQRKAEEL 360

RESULT 8

US-08-557-309B-37
 Sequence 37, Application US/08557309B
 Patent No. 5916572

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Lodes, Michael J.
 APPLICANT: Houghton, Raymond L.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
 NUMBER OF SEQUENCES: 69
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/557,309B
 FILING DATE: 14-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.422
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900

```
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-557-309B-37

Query Match 61.3%; Score 38; DB 2; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMORRADOLA 13
Db 367 EEMIRRAEELA 377

RESULT 9
US-08-834-306-37
; Sequence 37, Application US/08834306
; Patent No. 6054135
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-834-306-37

Query Match 61.3%; Score 38; DB 3; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMORRADOLA 13
Db 367 EEMIRRAEELA 377

RESULT 10
US-08-993-674A-37
; Sequence 37, Application US/08993674A
; Patent No. 6228372
```

```
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION OF T
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.422C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 639 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-993-674A-37

Query Match 61.3%; Score 38; DB 3; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMORRADOLA 13
Db 367 EEMIRRAEELA 377

RESULT 11
US-09-256-976-37
; Sequence 37, Application US/09256976
; Patent No. 6419933
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Smith, John M.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DETECTION AND PREVENTION
; FILE OF INVENTION: OF T. CRUZI INFECTION
; FILE REFERENCE: 210121.422C3
; CURRENT APPLICATION NUMBER: US/09/256,976
; CURRENT FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
; FEATURE:
; OTHER INFORMATION: Where any Xaa is an independently selected amino
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```
; OTHER INFORMATION: acid
US-09-256-976-37

Query Match      61.3%; Score 38; DB 4; Length 639;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EEMORRADOLA 13
DB 367 EEMIRRAEELA 377

RESULT 12
US-09-252-991A-22550
; Sequence 22550, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22550
; LENGTH: 931
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22550

Query Match      61.3%; Score 38; DB 4; Length 931;
Best Local Similarity 63.6%; Pred. No. 3.3e+02;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ELEMORRADQ 11
DB 601 QVEBQRQADQ 611

RESULT 13
US-09-489-039A-13840
; Sequence 13840, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13840
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13840

Query Match      59.7%; Score 37; DB 4; Length 513;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 LEEMORRADOLA 13
DB 101 LREMQRYDQAA 112

RESULT 14
US-09-229-007A-96
; Sequence 96, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; TITLE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preselcted Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:ZFP sequence
; OTHER INFORMATION: (F1, F2, F3) from SPI
US-09-229-007A-96

Query Match      58.1%; Score 36; DB 4; Length 21;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 BEMORRADOLA 13
DB 10 DELQRSDDL 20

RESULT 15
US-09-252-991A-24357
; Sequence 24357, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24357
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24357

Query Match      58.1%; Score 36; DB 4; Length 171;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEEMORRADQ 11
DB 87 LEQFORRLDQ 96

Search completed: March 4, 2004, 08:31:46
Job time : 22.8947 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 69.1053 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-10-030-485A-3
Perfect score: 62
Sequence: 1 ELEEMQRRADQLA 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	100.0	13	AAB15583	Aab15583 Human SNA
2	62	100.0	64	AAG00764	Aag00764 Human sec
3	62	100.0	82	AAB15581	Aab15581 Human SNA
4	62	100.0	106	AAG03825	Aag03825 Human sec
5	62	100.0	106	AAG03826	Aag03826 Human sec
6	62	100.0	198	AAU00255	Aau00255 Synaptoso
7	62	100.0	199	AAU00263	Aau00263 Synaptoso
8	62	100.0	200	AAU00264	Aau00264 Synaptoso
9	62	100.0	201	AAU02637	Aau02637 Synaptoso
10	62	100.0	202	AAU00265	Aau00265 Synaptoso
11	62	100.0	203	AAU02636	Aau02636 Synaptoso
12	62	100.0	206	AAW30103	Aaw30103 Synaptoso
13	62	100.0	206	AAW43426	Aaw43426 Mouse syn
14	62	100.0	206	AAW79198	Aaw79198 Mouse SNA
15	62	100.0	206	AAU00256	Aau00256 Synaptoso
16	62	100.0	206	AAU00261	Aau00261 Synaptoso
17	62	100.0	206	AAU00246	Aau00246 Synaptoso
18	62	100.0	206	AAU00253	Aau00253 SNARE hom
19	62	100.0	206	AAU02171	Aau02171 Synaptoso
20	62	100.0	206	AAU00266	Aau00266 Synaptoso
21	62	100.0	206	AAU02640	Aau02640 Synaptoso
22	62	100.0	206	AAU00258	Aau00258 Synaptoso
23	62	100.0	206	AAU00262	Aau00262 Synaptoso
24	62	100.0	206	AAU00259	Aau00259 Synaptoso
25	62	100.0	206	AAU00252	Aau00252 SNARE hom

26	62	100.0	206	4	AAU00260	Aau00260 Synaptoso
27	62	100.0	206	4	AAU02638	Aau02638 Synaptoso
28	62	100.0	206	4	AAU02639	Aau02639 Synaptoso
29	62	100.0	206	6	AAU00257	Aau00257 Synaptoso
30	62	100.0	206	6	AAE36662	Aae36662 Human SNA
31	62	100.0	206	6	AAE36667	Aae36667 Rat VAMP-
32	62	100.0	206	7	ADE54280	Ade54280 Rat Prote
33	62	100.0	206	7	ADE54288	Ade54288 Rat Prote
34	62	100.0	206	7	ADE54276	Ade54276 Rat Prote
35	62	100.0	206	7	ADE54290	Ade54290 Human Pro
36	62	100.0	206	7	ADE54282	Ade54282 Rat Prote
37	62	100.0	206	7	ADE54274	Ade54274 Rat Prote
38	62	100.0	206	7	ADE54286	Ade54286 Human Pro
39	62	100.0	206	7	ADE54284	Ade54284 Rat Prote
40	62	100.0	206	7	ADE54272	Ade54272 Rat Prote
41	62	100.0	206	7	ADE54278	Ade54278 Rat Prote
42	44	71.0	252	5	ABP25533	Abp25533 Streptoco
43	44	71.0	252	6	ABU46723	Abu46723 Protein e
44	41	66.1	480	4	AAB96534	Aab96534 Putative
45	40	64.5	312	5	ABB78803	Abb78803 Intermedi

ALIGNMENTS

RESULT 1
AAB15583
ID AAB15583 standard; peptide; 13 AA.
XX
AC AAB15583;
XX
DT 02-MAR-2001 (first entry)
XX
DE Human SNAP-25 N-terminal peptide #3.
XX
KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.
XX
OS Homo sapiens.
XX
FN WC2000064932-A1.
XX
PD 02-NOV-2000.
XX
PF 18-FEB-2000; 2000WO-ES000058.
XX
PR 23-APR-1999; 99ES-00000844.
XX
PI (LIPO-) LIPOTEC SA.
XX
PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
PI Perez Paya E;
XX
DR WPI; 2001-007091/01.
XX
PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.
XX
FS Claim 9; Page 32; 40pp; Spanish.
XX
CC The invention relates to new peptides comprising 3-10 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders
XX
SQ Sequence 13 AA;

Query Match 100.0%; Score 62; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMORRADOLA 13
 |||||
 DB 1 ELEEMORRADOLA 13

RESULT 2
 AAG00764
 ID AAG00764 standard; protein, 64 AA.
 XX
 AC AAG00764;
 XX
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 4845.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 PA
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI: 2000-500381/45.
 DR N-PSDB; AAC00770.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.
 PS
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 XX Sequence 64 AA;
 SQ

Query Match 100.0%; Score 62; DB 3; Length 64;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMORRADOLA 13
 |||||
 DB 10 ELEEMORRADOLA 22

RESULT 3
 AAB15581
 ID AAB15581 standard; peptide, 82 AA.
 XX
 AC AAB15581;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Human SNAP-25 N-terminal peptide #1.
 XX
 KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
 KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
 KW neurodegenerative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200064932-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 18-FEB-2000; 2000WO-ES000058.
 XX
 PR 23-APR-1999; 99ES-00000844.
 XX
 XX (LIPO-) LIPOTEC SA.
 PA
 PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
 PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
 PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
 PI Perez Paya E;
 XX
 DR WPI: 2001-007091/01.
 XX
 XX New peptides containing amino acid sequences from known proteins for
 PT treatment of neurological disorders.
 PT
 XX Claim 1; Page 31; 40pp; Spanish.
 PS
 CC The invention relates to new peptides comprising 3-30 contiguous amino
 CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
 CC protein 25). The peptides AAB15581-B15586 represent examples of the
 CC peptides of the invention. The peptides have neuronal exocytosis
 CC inhibitory activity and are used for treatment of facial wrinkles and
 CC asymmetry and pathological neuronal exocytosis-mediated pathological
 CC disorders and alterations manifested e.g. by spasms and neurological and
 CC neurodegenerative disorders
 XX
 XX Sequence 82 AA;
 SQ

Query Match 100.0%; Score 62; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEEMORRADOLA 13
 |||||
 DB 9 ELEEMORRADOLA 21

RESULT 4
 AAG03825
 ID AAG03825 standard; protein, 106 AA.
 XX
 AC AAG03825;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 7906.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX

PD 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000EP-00200610.
 XX
 XX 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 XX N-PSDB; AAC03831.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.
 XX
 XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 XX Sequence 106 AA;
 SQ
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 XX Sequence 106 AA;
 SQ
 Query Match 100.0%; Score 62; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. NO. 0.043;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 |||||
 Db 10 ELEMORRADQLA 22
 |||||
 RESULT 5
 AAG03826
 ID AAG03826 standard; protein; 106 AA.
 AC AAG03826;
 XX
 XX 06-OCT-2000 (first entry)
 DT
 XX Human secreted protein, SEQ ID NO: 7907.
 DE
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 KW Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-00200610.
 PF
 XX 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 XX N-PSDB; AAC03832.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.
 XX
 XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 XX Sequence 106 AA;
 SQ
 Query Match 100.0%; Score 62; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. NO. 0.043;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 |||||
 Db 10 ELEMORRADQLA 22
 |||||
 RESULT 6
 AAU00255
 ID AAU00255 standard; protein; 198 AA.
 AC AAU00255;
 XX
 XX 12-SEP-2001 (first entry)
 DT
 XX Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
 DE
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 XX Mus sp.
 OS Synthetic.
 XX WO200118038-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX 18-AUG-2000; 2000WO-GB003196.
 PF
 XX 20-AUG-1999; 99US-0149993P.
 PR
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 PA
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 DR
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 PS
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
 CC

CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the
 CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state. Note: The present sequence is
 CC not shown in the specification but is derived from the mouse SNAP-25
 CC sequence given in figure 8 (see AAU00246)
 XX
 SQ Sequence 198 AA;

Query Match 100.0%; Score 62; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
 |||||
 DB 10 ELEMORRADOLA 22

RESULT 7
 AAU00263
 ID AAU00263 standard; protein; 199 AA.
 AC AAU00263;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-199 (R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 FN
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a

PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 PS Example 1; Page; 13pp; English.

XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199 (R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 199 AA;

Query Match 100.0%; Score 62; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 0.078;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELEMORRADOLA 13
 |||||
 DB 10 ELEMORRADOLA 22

RESULT 8
 AAU00264
 ID AAU00264 standard; protein; 200 AA.
 AC AAU00264;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Synaptosomal-associated protein, SNAP25, mutant 1-200 (R198T).
 XX
 KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 FN
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a

PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 200 AA;
 XX
 XX Query Match 100.0%; Score 62; DB 4; Length 200;
 XX Best Local Similarity 100.0%; Pred. No. 0.078;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ELEMQRADQLA 13
 XX |||||
 XX Db 10 ELEMQRADQLA 22
 XX
 XX RESULT 9
 XX AAU02637
 XX ID AAU02637 standard; protein; 201 AA.
 XX AC AAU02637;
 XX
 XX DT 12-SEP-2001 (first entry)
 XX
 XX DE Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; mouse; mutant; mutein;
 XX N-ethylmaleimide-sensitive fusion protein;
 XX soluble NSF-attachment protein receptor.
 XX
 XX OS Mus sp.
 XX OS Synthetic.
 XX
 XX PH Key Location/Qualifiers
 XX FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 XX
 XX PN WO200118038-A2.

XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 XX Sequence 201 AA;
 XX
 XX Query Match 100.0%; Score 62; DB 4; Length 201;
 XX Best Local Similarity 100.0%; Pred. No. 0.079;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ELEMQRADQLA 13
 XX |||||
 XX Db 10 ELEMQRADQLA 22
 XX
 XX RESULT 10
 XX AAU00265
 XX ID AAU00265 standard; protein; 202 AA.
 XX AC AAU00265;
 XX
 XX DT 12-SEP-2001 (first entry)
 XX
 XX DE Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; mouse; mutant; mutein;
 XX N-ethylmaleimide-sensitive fusion protein;
 XX soluble NSF-attachment protein receptor.
 XX
 XX OS Mus sp.

OS Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 FT
 XX
 XX
 XX W0200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 202 AA;
 Query Match 100.0%; Score 62; DB 4; Length 202;
 Best Local Similarity 100.0%; Pred. No. 0.079;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 DB 10 ELEMORRADQLA 22
 |||||
 RESULT 11
 AAU02636
 ID AAU02636 standard; protein; 203 AA.
 XX AC
 XX AAU02636;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 XX Synaptosomal-associated protein, SNAP25, mutant 1-203 (R198T).
 XX

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; muclein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 198
 FT /note= "Wild-type Arg substituted by Thr"
 FT
 XX
 XX W0200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-203(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX
 SQ Sequence 203 AA;
 Query Match 100.0%; Score 62; DB 4; Length 203;
 Best Local Similarity 100.0%; Pred. No. 0.08;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 DB 10 ELEMORRADQLA 22
 |||||
 RESULT 12
 AAU03103
 ID AAU03103 standard; peptide; 206 AA.

XX AAW30103;
 AC
 XX 06-APR-1998 (first entry)
 DT
 XX Synaptosomal associated protein.
 DE
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 XX WO9734620-A1.
 PN
 XX 25-SEP-1997.
 PD
 XX 18-MAR-1997; 97WO-US004393.
 PF
 XX 18-MAR-1996; 96US-0013599P.
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Montal M;
 PI
 XX WPI; 1997-479986/44.
 DR
 XX Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 FT
 XX Disclosure: Page 27-28; 61pp; English.
 PS
 XX This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitory agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microM, especially 0.25 microM, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provide targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEEMORRADOLA 13
 Db 10 ELEEMORRADOLA 22
 RESULT 13
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX AAW43426;
 AC
 XX 27-APR-1998 (first entry)
 DT
 XX Mouse synaptosomal-associated protein-25.
 DE
 XX

KW Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 XX neurodegenerative disease; hormonal disorder; immunological disorder.
 OS Mus sp.
 XX US5693476-A.
 PN
 XX 02-DEC-1997.
 PD
 XX 24-FEB-1995; 95US-00393985.
 PF
 XX 24-FEB-1995; 95US-00393985.
 PR
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA
 XX Scheller RH;
 PI
 XX WPI; 1998-031743/03.
 DR
 XX N-PSDB; AAV01554.
 XX
 XX Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 FT
 XX Disclosure: Col 67-72; 57pp; English.
 PS
 XX This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 62; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.081;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEEMORRADOLA 13
 Db 10 ELEEMORRADOLA 22
 RESULT 14
 AAW79198
 ID AAW79198 standard; protein; 206 AA.
 XX
 AC AAW79198;
 XX
 XX 25-NOV-1998 (first entry)
 DT
 XX Mouse SNAP-25 polypeptide.
 DE
 XX Hrs-2 polypeptide; ATP-preferring nucleotidase; SNAP-25; vesicle docking;
 KW calcium-regulated secretion; secretory vesicle; secretory process; brain;
 KW neurotransmitter release; presynaptic membrane; CNS disorder; depression;
 KW Parkinson's disease; endocrine system; hormonal imbalance; cell division;
 KW thought disorder; schizophrenia; degenerative disorder; anaesthesia; rat;
 KW immune system; antigen processing; immunomodulator; viral processing;
 KW central nervous system; vesicular release; affective disorder; human;
 KW anti-tumour application; membrane trafficking regulation; mouse.
 XX
 OS Mus sp.
 XX WO9838210-A2.
 PN
 XX

PD 03-SEP-1998.
 XX
 XX 26-FEB-1998; 98WO-US003789.
 XX
 XX 26-FEB-1997; 97US-0039159P.
 XX
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Bean AJ, Scheller RH;
 XX
 XX WPI; 1998-481140/41.
 XX
 XX N-PSDB; AAV57558.
 XX
 XX New isolated Hrs-2 nucleotidase - used in assays to identify compounds
 XX capable of modulating calcium-regulatory secretion of secretory vesicles,
 XX such as in neurotransmitter release.
 XX
 XX Claim 16; Page 42-44; 55pp; English.
 XX
 XX This represents a mouse SNAP-25 polypeptide, a component of the protein
 XX polypeptides thought to underlie vesicle docking and fusion. The
 XX invention provides rat and human Hrs-2 polypeptides which are ATP-
 XX preferring nucleotidase that associate with SNAP-25. For identifying a
 XX compound capable of modulating calcium-regulated secretion of secretory
 XX vesicles, a SNAP-25 polypeptide can be contacted with a Hrs-2
 XX polypeptide, in the presence and absence of a test compound. The effect
 XX of the test compound on the extent of binding between the SNAP-25 and Hrs
 XX -2 polypeptides are measured and a compound is identified as effective if
 XX its measured effect on the extent of binding is above a threshold level.
 XX The products can be used for identifying drugs capable of affecting
 XX secretory processes, such as neurotransmitter release at the active zones
 XX of presynaptic membranes. Such drugs can be used for treating disorders
 XX or conditions of the central nervous system by selectively enhancing or
 XX inhibiting vesicular release in specific areas of the brain, including
 XX affective disorders (e.g. depression), disorders of thought (e.g.
 XX schizophrenia) and degenerative disorders (Parkinson's disease), as well
 XX as applications such as anaesthesia. The drugs can also be used
 XX therapeutically in other systems such as the endocrine system for
 XX treatment of hormonal imbalances, the immune system for intervention in
 XX antigen processing, secreted immunomodulators, and viral processing, as
 XX well as anti-tumour applications, such as regulation of membrane
 XX trafficking during rapid cell division
 XX
 XX Sequence 206 AA;
 XX
 XX Query Match 100.0%; Score 62; DB 2; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 0.081;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 Db |||||
 10 ELEMORRADQLA 22
 RESULT 15
 AAU00256
 ID AAU00256 standard; protein; 206 AA.
 XX
 XX AAU00256;
 XX
 XX 12-SEP-2001 (first entry)
 XX
 XX Synaptosomal-associated protein, SNAP25, mutant Q197A/R198A.
 XX
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 XX toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 XX synaptosomal-associated protein; mouse; mutant; mutin;
 XX N-ethylmaleimide-sensitive fusion protein;
 XX soluble NSF-attachment protein receptor.
 XX
 XX Mus sp.
 XX Synthetic.
 XX

FH Key Location/Qualifiers
 FT Misc-difference 197 /note= "Wild-type Gln substituted by Ala"
 FT Misc-difference 198 /note= "Wild-type Arg substituted by Ala"
 XX
 XX WO200118038-A2.
 XX
 XX 15-MAR-2001.
 XX
 XX 18-AUG-2000; 2000WO-GB003196.
 XX
 XX 20-AUG-1999; 99US-0149993P.
 XX
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX
 XX Dolly JO, O'Sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, e.g. botulism, comprises administering a toxin-
 XX resistant or toxin-inhibitory SNARE.
 XX
 XX Example 1; Page; 131pp; English.
 XX
 XX The sequence represents the amino acid sequence of synaptosomal-
 XX associated protein, SNAP25, mutant Q197A/R198A, used in a new method of
 XX treating a patient suffering from poisoning or at risk of poisoning by a
 XX clostridial toxin, comprising supplying a SNARE (soluble N-
 XX ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 XX a cell of the patient, where the SNARE is resistant to proteolysis by the
 XX toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 XX (toxin-inhibitory SNARE). The protein can be used in a method of treating
 XX a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 XX capable of performing SNARE-dependent exocytosis, comprises supplying a
 XX fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 XX to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 XX or a recombinant polynucleotide encoding the SNARE is useful in the
 XX manufacture of a medicament for the treatment of a patient suffering from
 XX poisoning or at risk of poisoning by clostridial toxin, e.g. from
 XX botulism or tetanus. The fragment, variant, fusion or derivative of a
 XX SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 XX either of these SNARE polypeptides are useful in the manufacture of
 XX medicament for the treatment of a patient in need of inhibition of SNARE-
 XX dependent exocytosis from a cell capable of performing SNARE-dependent
 XX exocytosis. The method of treatment is relatively fast, thus alleviating
 XX the symptoms when most severe and taking the patient out of critical
 XX state. Note: The present sequence is not shown in the specification but
 XX is derived from the mouse SNAP-25 sequence given in figure 8 (see
 XX AAU00246)
 XX
 XX Sequence 206 AA;
 XX
 XX Query Match 100.0%; Score 62; DB 4; Length 206;
 XX Best Local Similarity 100.0%; Pred. No. 0.081;
 XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELEMORRADQLA 13
 Db |||||
 10 ELEMORRADQLA 22
 Search completed: March 4, 2004, 08:27:50
 Job time : 70.1053 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 6.63158 Seconds
(without alignments)
47.111 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt.42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	30	100.0	206	1 SN25 HUMAN	P13795 homo sapien
2	27	90.0	180	1 STN3 CHICK	Q93388 gallus gall
3	27	90.0	219	1 IF6 METMA	Q8YQY3 methanosarc
4	27	90.0	303	1 PQOB PSEPL	P55172 pseudomonas
5	27	90.0	303	1 PQOB PSEPK	Q88GV5 pseudomonas
6	27	90.0	303	1 PQOB PSESM	Q88A81 pseudomonas
7	27	90.0	328	1 CORA COREP	Q8FQZ2 corynebacte
8	27	90.0	388	1 LHX9 HUMAN	Q9NQS9 homo sapien
9	27	90.0	388	1 LHX9 MOUSE	Q9WU22 mus musculu
10	27	90.0	390	1 TFT1 MOUSE	Q08970 mus musculu
11	27	90.0	450	1 PUR8 PYRAB	Q9U299 pyrococcus
12	27	90.0	450	1 PUR8 PYRHO	O58582 pyrococcus
13	27	90.0	509	1 GATB TREPA	O83984 treponema p
14	27	90.0	568	1 ESR2 ONCMY	P57782 oncorhynch
15	27	90.0	613	1 ILVD CORGL	Q8NG93 corynebacte
16	27	90.0	622	1 YAE7 YEAST	P39723 saccharomyc
17	27	90.0	636	1 PAPB HUMAN	Q9WV66 mus musculu
18	27	90.0	641	1 PAPB MOUSE	Q9WV66 mus musculu
19	27	90.0	660	1 PAP HUMAN	P51003 homo sapien
20	27	90.0	677	1 GCF3 MOUSE	P58854 mus musculu
21	27	90.0	727	1 YM29 YEAST	Q03792 saccharomyc
22	27	90.0	738	1 PAP BOVIN	P25500 bos taurus
23	27	90.0	738	1 PAP MOUSE	Q61183 mus musculu
24	27	90.0	809	1 HEL1 EBV	P03214 epstein-bar
25	27	90.0	907	1 GCP3 HUMAN	Q96CW5 homo sapien
26	27	90.0	960	1 FGD1 MOUSE	P52734 mus musculu
27	27	90.0	961	1 FGD1 HUMAN	P98174 homo sapien
28	27	90.0	1052	1 BULB MOUSE	Q9Z180 mus musculu
29	27	90.0	2133	1 FAF FIG	P12263 sus scrofa
30	26	86.7	200	1 RH02 SCHPO	Q10133 schizosacch
31	26	86.7	204	1 SNXN HUMAN	Q96193 homo sapien
32	26	86.7	261	1 NEF SVLSP	P19501 simian immu
33	26	86.7	340	1 ADHA RHIME	Q31186 rhizobium m

RESULT 1																		
ID	SN25_HUMAN	STANDARD;	PRT;	206 AA.														
AC	P13795;	P36974;	P70557;	P70558;	Q8IXK3;	Q96FM2;	Q9BR45;											
DT	01-JAN-1990	(Rel. 13, Created)																
DT	01-FEB-1991	(Rel. 17, Last sequence update)																
DT	15-MAR-2004	(Rel. 43, Last annotation update)																
DE	Synaptosomal-associated protein 25 (SNAP-25) (Super protein) (SUP).																	
GN	SNAP25 OR SNAP.																	
OS	Homo sapiens (Human),																	
OS	Macaca mulatta (Rhesus macaque),																	
OS	Mus musculus (Mouse),																	
OS	Rattus norvegicus (Rat), and																	
OS	Gallus gallus (Chicken).																	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.																	
OX	NCBI_TaxID=9606, 9544, 10090, 10116, 9031;																	
RN	[1]																	
RP	SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).																	
RC	SPECIES=Human; TISSUE=Brain;																	
RX	MEDLINE=94156217; PubMed=8112622;																	
RA	Bark I.C., Wilson M.C.;																	
RT	"Human cDNA clones encoding two different isoforms of the nerve																	
RT	terminal protein SNAP-25.";																	
RL	Gene 139:291-292(1994).																	
RN	[2]																	
RP	SEQUENCE FROM N.A. (ISOFORMS SNAP-25A).																	
RC	SPECIES=Human; TISSUE=Brain;																	
RX	MEDLINE=94333829; PubMed=8056350;																	
RA	Zhao N., Hashida H., Takahashi N., Sakaki Y.;																	
RT	"Cloning and sequence analysis of the human SNAP25 cDNA.";																	
RL	Gene 145:313-314(1994).																	
RN	[3]																	
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.																	
RC	SPECIES=Human; TISSUE=Skeletal muscle;																	
RX	MEDLINE=96332494; PubMed=8760387;																	
RA	Jagadeish M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Alafaci A.,																	
RA	Gough K.H., Grusovin J., Verkuylen A., Cosgrove L.,																	
RA	Frenkel M.J., Ward C.W.;																	
RT	"Insulin-responsive tissues contain the core complex protein SNAP-25																	
RT	(synaptosomal-associated protein 25) A and B isoforms in addition to																	
RT	syntaxin 4 and synaptobrevins 1 and 2.";																	
RL	Biochem. J. 317:945-954(1996).																	
RN	[4]																	
RP	SEQUENCE FROM N.A.																	
RC	SPECIES=Human;																	
RX	MEDLINE=21638749; PubMed=11780052;																	
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,																	
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,																	
RA	Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,																	
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,																	
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,																	
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,																	
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,																	
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,																	
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,																	

015995 hemicentrot
019895 caenorhabdi
P48062 bordetella
Q881f6 pseudomonas
Q884c8 pseudomonas
P05429 synchocyst
Q35345 mus musculu
Q9uin0 chironomus
Q9hcd5 homo sapien
Q91w39 mus musculu
Q65947 canine aden
Q8u0w9 pyrococcus

ALIGNMENTS

- RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliland R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt S.E., Jekes K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslalo M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McIlroy K., McMurray A.A.,
RA Milne S.K., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.W., Ross M.F., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.B., Soderlund C., Stewart C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tyanom A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilning L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.,
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
[5]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Human; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Teshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=M.mullatta; TISSUE=Hippocampus;
RA Jensen M.J., Smith L.A.,
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[7]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=BALB/c;
RX MEDLINE=90078337; PubMed=2592413;
RA Oyler G.A., Higgins G.A., Hart R.A., Battenberg E., Billingsley M.,
RA Bloom F.E., Wilson M.C.,
RT "The identification of a novel synaptosomal-associated protein,
RT SNAP-25, differentially expressed by neuronal subpopulations.";
RL J. Cell Biol. 109:3039-3052(1989).
[8]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=ILS and ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Eringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.,
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related QTLs.";
RL Mamm. Genome 12:657-663(2001).
[9]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25B).
RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX MEDLINE=22354683; PubMed=12466811;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Buit C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmel S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[10]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Mouse; STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.L.,
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[11]
RP SEQUENCE FROM N.A. (ISOFORMS SNAP-25A AND SNAP-25B).
RC SPECIES=Cat;
RA Kataoka M.,
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[12]
RP SEQUENCE FROM N.A. (ISOFORM SNAP-25A).
RC SPECIES=Cat; TISSUE=Brain;
RA Cho A.R., You K.H.,
RT "Cloning of the SNAP-25 gene from a rat brain cDNA library.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[13]
RP SEQUENCE OF 10-190 FROM N.A. (ISOFORM SNAP-25B).
RC SPECIES=Cat; TISSUE=Brain;
RX MEDLINE=99155074; PubMed=10037470;
RA Madison D.L., Krueger W.H., Cheng D., Trapp B.D., Pfeiffer S.E.,
RT "SNARE complex proteins, including the cognate pair VAMP-2 and
RT syntaxin-4, are expressed in cultured oligodendrocytes.";
RL J. Neurochem. 72:988-998(1999).
[14]
RP SEQUENCE FROM N.A.
RC SPECIES=Chicken; TISSUE=Retina;
RX MEDLINE=91126080; PubMed=1992470;
RA Calsicas S., Lathammar D., Blomqvist A.G., Sanna P.P., Milner R.J.,
RA Wilson M.C.,
RT "Expression of a conserved cell-type-specific protein in nerve
RT terminals coincides with synaptogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:785-789(1991).
[15]
RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.
RC SPECIES=Chicken;
RX MEDLINE=93389738; PubMed=8377193;
RA Bark I.C.,
RT "Structure of the chicken gene for SNAP-25 reveals duplicated exon
RT encoding distinct isoforms of the protein.";
RL J. Mol. Biol. 233:67-76(1993).
[16]
RP PALMITOYLATION.
RC SPECIES=Cat;
RX MEDLINE=93100552; PubMed=1281490;
RA Hess D.T., Slater T.M., Wilson M.C., Skene J.H.P.,
RT "The 25 kDa synaptosomal-associated protein SNAP-25 is the major
RT methionine-rich polypeptide in rapid axonal transport and a major

```

Query Match      100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
   |||||
Db 12 EEMQRR 17

RESULT 2
ID STN3 CHICK STANDARD; PRT; 180 AA.
AC O93388;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Stathmin 3 (SCG10-like protein) (Neuroplasticin-2).
GN STN3 OR SCLIP OR NPC2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lutjens R., Osen-Sand A., Grenningloh G.;
RT "Characterization of a new member of the SCG10/stathmin family of
   genes.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the stathmin family.
CC
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CC
CC EMBL; AF076982; AAC27325.1; -.
DR InterPro; IPR000956; Stathmin.
DR Pfam; PF00836; Stathmin; 1.
DR PRINTS; PR00345; STATHMIN.
DR PROSITE; PS00563; STATHMIN_1; 1.
DR PROSITE; PS01041; STATHMIN_2; 1.
KW Coiled coil. 75 179 COILED COIL (POTENTIAL).
FT DOMAIN 180 AA; 20994 MW; DE3554B4E8BDEF5E CRC64;
SQ SEQUENCE 180 AA; 20994 MW; DE3554B4E8BDEF5E CRC64;

Query Match      90.0%; Score 27; DB 1; Length 180;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
   |||||
Db 83 EELQRR 88

RESULT 3
ID IF6 METWA STANDARD; PRT; 219 AA.
AC Q8FYQ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Translation initiation factor 6 (aIF-6).
GN EIF6 OR M0807.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanococcus; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC STRAIN=Goel / Goel / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824; Merk R., Schmitz R.A.,
RA Deppenmeier U., Johann A., Hartsch T., Merk R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Baeuer A., Baeuer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
   transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
CC -!- FUNCTION: Binds to the 60S ribosomal subunit and prevents its
   association with the 40S ribosomal subunit to form the 80S
   initiation complex (By similarity).
CC -!- SIMILARITY: Belongs to the eIF-6 family.
CC
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CC
CC EMBL; AE013306; AAM30503.1; -.
DR HAMAP; MF 00032; -.
DR InterPro; IPR002769; eIF6.
DR Pfam; PF01912; eIF6; 1.
DR ProDom; PD006880; eIF6; 1.
KW Initiation factor; Protein biosynthesis; Complete proteome.
KX SEQUENCE 219 AA; 23114 MW; 06E0E1FC24FDEF25 CRC64;
SQ SEQUENCE 219 AA; 23114 MW; 06E0E1FC24FDEF25 CRC64;

Query Match      90.0%; Score 27; DB 1; Length 219;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
   |||||
Db 77 EEMQRR 82

RESULT 4
ID PQOB PSEFL STANDARD; PRT; 303 AA.
AC P55172;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
   biosynthesis protein B).
DE PQOB.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHA0;
RX MEDLINE=96064397; PubMed=8526497;
RA Schneider U., Keel C., Defago G., Haas D.;
RT "Tns-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:
   mutational inactivation of the genes results in overproduction of the
   antibiotic pyoluteorin.";
RA Appl. Environ. Microbiol. 61:3856-3864 (1995).
CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
   to the periplasm (By similarity).
CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
CC -!- SIMILARITY: Belongs to the pqqB family.
CC
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DR EMBL; X87299; CA60733.1; -;
 DR PIR; S58243; 558243.
 DR HAMAP; MF 00653; -; 1.
 KW PQQ biosynthesis; Transport.
 SQ SEQUENCE 303 AA; 33207 MW; 8D958BD1A9CD32F9 CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||
 DB 227 DEMQRR 232

RESULT 5
 PQQB_PSEPK STANDARD; PRT; 303 AA.
 AC Q8QV5; 558243.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
 biosynthesis protein B).
 DE PQQB OR PP0379.
 GN Pseudomonas putida (strain KT2440).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=160488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;
 RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson M., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
 RA Uterback T., Rizzo M., Lee K., Kosack D., Moesti D., Wedler H.,
 RA Lauber J., Stjepandic D., Hohnsbeil J., Straetz M., Heim S.,
 RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
 CC to the periplasm (By similarity).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqB family.

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DR EMBL; AE016775; AAN6010.1; -;
 DR TIGR; PP0379; -;
 DR HAMAP; MF 00653; -; 1.
 KW PQQ biosynthesis; Transport; Complete proteome.
 SQ SEQUENCE 303 AA; 33331 MW; 37A3653C65B52B01E CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||

DB 227 DEMQRR 232

RESULT 6
 PQQB_PSESM STANDARD; PRT; 303 AA.
 AC Q8BA81; 558243.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Coenzyme PQQ synthesis protein B (Pyrroloquinoline quinone
 biosynthesis protein B).
 DE PQQB OR PSPT00512.
 GN Pseudomonas syringae (pv. tomato).
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
 RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
 RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T., Zafar N., Zhou L., Liu J., Yuan Q.,
 RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Uterback T.,
 RA Van Aken S.E., Feldblyum T.V., D'Acenzio M., Deng W.-L., Ramos A.R.,
 RA Alfano J.R., Cartinour S., Chatterjee A.K., Delaney T.P.,
 RA Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
 RA White O., Fraser C.M., Collier A.;
 RT "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 CC -!- FUNCTION: May be involved in the transport of PQQ or its precursor
 CC to the periplasm (By similarity).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqB family.

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DR EMBL; AE016857; AAO54055.1; -;
 DR TIGR; PSPT00512; -; 1.
 DR HAMAP; MF 00653; -; 1.
 KW PQQ biosynthesis; Transport; Complete proteome.
 SQ SEQUENCE 303 AA; 33326 MW; 2B6C41E02AF016CC CRC64;

Query Match 90.0%; Score 27; DB 1; Length 303;
 Best Local Similarity 83.3%; Pred. No. 98;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 :|||||
 DB 227 DEMQRR 232

RESULT 7
 CORA_COREF STANDARD; PRT; 328 AA.
 ID CORA_COREF
 AC Q8F0R2; 558243.
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Pantothate kinase (EC 2.7.1.33) (Pantothenic acid kinase).
 DE CORA OR CB1057.
 GN Corynebacterium efficiens.
 OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Corynebacteriidae; Corynebacterium.

```

OX NCBI_TaxID=152794;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RX MEDLINE=22723752; PubMed=12840036;
RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens.";
RL Genome Res. 13:1572-1579(2003).
CC -|- CATALYTIC ACTIVITY: ATP + pantothenate = ADP + D-4'-
CC phosphopantothenate.
CC -|- PATHWAY: Coenzyme A (CoA) biosynthesis; first step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -|- SIMILARITY: Belongs to the prokaryotic pantothenate kinase family.
CC
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CC
CC -----
CC EMBL; AP005217; BAC17867.1; -.
CC HAMAP; MF 00215; -. 1.
CC InterPro; IPR004566; Pank.bact.
CC InterPro; IPR006083; PRK_UNK.
CC Pfam; PF00485; PRK; 1.
CC PIRSF; PIRSF000545; Pantothenate kin; 1.
CC TIGRFAMs; TIGR00554; pank.bact; 1.
CC Transferase; Kinase; ATP-binding; Coenzyme A biosynthesis;
CC Complete proteome.
CC NP_BIND 113 120 ATP (POTENTIAL).
CC SEQUENCE 328 AA; 37254 MW; B6737A57964DC205 CRC64;
CC
CC Query Match 90.0%; Score 27; DB 1; Length 328;
CC Best Local Similarity 83.3%; Pred. No. 1.1e+02;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EMOQR 6
CC |||:|
CC 152 EELQRR 157
CC
CC RESULT 8
CC LHX9 HUMAN
CC ID LHX9_HUMAN STANDARD; PRT; 388 AA.
CC AC Q9N069; Q9BYU6; Q9NQ70;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE LIM/homeobox protein Lhx9.
CC GN LHX9.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Testis;
CC MEDLINE=21291005; PubMed=11397841;
CC RA Ottolenghi C., Moreira-Filho C., Mendonca B.B., Barbieri M.,
CC RA Fellous M., Berkovitz G.D., McElreavey K.;
CC RT "Absence of mutations involving the LIM homeobox domain gene LHX9 in
CC 46,Xf gonadal agenesis and dysgenesis.";
CC RL J. Clin. Endocrinol. Metab. 86:2465-2469(2001).
CC -|- FUNCTION: Involved in gonadal development (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -|- SIMILARITY: Contains 1 homeobox domain.
CC -|- SIMILARITY: Contains 2 LIM zinc-binding domains.

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CC
CC -----
CC EMBL; AJ277915; CAB97493.1; -.
CC EMBL; AJ277916; CAB98128.1; ALT SEQ.
CC EMBL; AJ277917; CAB98128.1; JOINED.
CC EMBL; AJ277918; CAB98128.1; JOINED.
CC EMBL; AJ277919; CAB98128.1; JOINED.
CC EMBL; AJ277920; CAB98128.1; JOINED.
CC EMBL; AJ277920; CAB98128.1; JOINED.
CC EMBL; AJ296272; CAB33174.1; -.
CC HSFP; P06601; 1FUL.
CC Genew; HGNC:14222; LHX9.
CC MIM; 606066; -.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR001781; LIM
CC InterPro; IPR001707; LIM homeo.
CC Pfam; PF00046; homeobox; 1.
CC Pfam; PF00412; LIM; 2.
CC ProDom; PD000010; Homeobox; 1.
CC ProDom; PD000094; LIM; 2.
CC SMART; SM00389; HOX; 1.
CC SMART; SM00132; LIM; 2.
CC PROSITE; PS00478; LIM_DOMAIN_1; 2.
CC PROSITE; PS50023; LIM_DOMAIN_2; 2.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS50071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
CC Metal-binding; zinc.
CC DOMAIN 62 114 LIM 1.
CC DOMAIN 124 177 LIM 2.
CC DOMAIN BIND 258 317 HOMEBOX.
CC SEQUENCE 388 AA; 42903 MW; A4DC8B914D7C3B66 CRC64;
CC
CC Query Match 90.0%; Score 27; DB 1; Length 388;
CC Best Local Similarity 83.3%; Pred. No. 1.3e+02;
CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 EMOQR 6
CC |||:|
CC 26 EEMERR 31
CC
CC RESULT 9
CC LHX9 MOUSE
CC ID LHX9_MOUSE STANDARD; PRT; 388 AA.
CC AC Q9WHZ2; Q9QY05; Q9QY06; Q9QZ00; Q9WU44;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE LIM/homeobox protein Lhx9.
CC GN LHX9.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE OF 1-300 FROM N.A.
CC RC STRAIN=C57BL/6;
CC MEDLINE=99098964; PubMed=9880598;
CC RA Retaux S., Rogard M., Bach I., Failli V., Besson M.J.;
CC RT "Lhx9: a novel LIM-homeobox domain gene expressed in the developing
CC forebrain.";
CC RL J. Neurosci. 19:783-793(1999).
CC [2]
CC RP SEQUENCE OF 11-388 FROM N.A.
CC RC STRAIN=NIH Swiss;
CC MEDLINE=99264291; PubMed=10330499;

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RA Bertuzzi S., Porter F.D., Pitts A., Kumar M., Agulnick A., Wassif C.,
 RA Westphal H.;
 RT "Characterization of Lhx9, a novel LIM/homeobox gene expressed by the
 RT pioneer neurons in the mouse cerebral cortex.";
 RL Mech. Dev. 81:193-198(1999).
 RN [3].
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=2021375; PubMed=10756098;
 RA Failli V., Rogard M., Mattei M.-G., Vernier P., Retaux S.;
 RT "Lhx9 and Lhx9alpha LIM-homeobox domain factors: genomic structure,
 RT expression patterns, chromosomal localization, and phylogenetic
 RT analysis.";
 RL Genomics 64:307-317(2000).
 RC -|- FUNCTION: Involved in gonadal development.
 CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -|- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Beta;
 CC IsoId=G9WUH2-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=G9WUH2-2; Sequence=VSP_003111;
 CC -|- SIMILARITY: Contains 1 homeobox domain.
 CC -|- SIMILARITY: Contains 2 LIM zinc-binding domains.
 CC -----
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 CC -----
 CC EMBL; AF134761; AAD30110.1; -;
 DR EMBL; AF113518; AAD22008.1; -;
 DR EMBL; AJ243851; CAB59907.1; -;
 DR EMBL; AJ243852; CAB59908.1; -;
 DR EMBL; AJ243853; CAB59908.1; JOINED.
 DR EMBL; AJ243854; CAB59908.1; JOINED.
 DR EMBL; AJ243855; CAB59908.1; JOINED.
 DR EMBL; AJ243856; CAB59908.1; JOINED.
 DR EMBL; AJ243857; CAB59909.1; -;
 DR EMBL; AJ243858; CAB59909.1; JOINED.
 DR EMBL; AJ243859; CAB59909.1; JOINED.
 DR EMBL; AJ243860; CAB59909.1; JOINED.
 DR EMBL; AJ243861; CAB59909.1; JOINED.
 DR HSP; P06601; IRLJ.
 DR TRANSFAC; T04192; -;
 DR TRANSFAC; T04195; -;
 DR MGD; MGI:1316721; Lhx9.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR001781; LIM.
 DR InterPro; IPR007107; LIM homeo.
 DR Pfam; PF00046; homeobox; 1.
 DR Pfam; PF00412; LIM; 2.
 DR ProDom; PD000010; Homeobox; 1.
 DR ProDom; PD000094; LIM; 2.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00132; LIM; 2.
 DR PROSITE; PS00027; HOMEBOX 1; 1.
 DR PROSITE; PS00071; HOMEBOX 2; 1.
 DR PROSITE; PS00478; LIM DOMAIN 1; 2.
 DR PROSITE; PS00028; LIM DOMAIN 2; 2.
 DR Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
 KW Metal-binding; Zinc; Alternative splicing.
 FT DOMAIN 62 114 LIM 1.
 FT DOMAIN 124 177 LIM 2.
 FT DNA_BIND 258 317 HOMEBOX.
 FT VARSPLIC 304 388 VWFQAFKFRNLRQENGVDKADGTSLEAPPSADSGAL
 FT TPPTGATTLTLNPTVTVTVTISNDSHPGPSQTTLT
 FT NLF -> GEQLGHYSQTSRLKIP (in isoform
 FT Alpha).
 FT /FTid=VSP_003111.

FT CONFLICT 49 49 A -> T (IN REF. 2).
 FT CONFLICT 153 153 S -> F (IN REF. 2).
 SQ SEQUENCE 388 AA; 42986 MW; C2D7326A68D87B32 CRC64;
 Query Match 90.0%; Score 27; DB 1; Length 388;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EMMORR 6
 DB 26 EMMERR 31
 RESULT 10
 TFFT1 MOUSE
 ID TFFT1 MOUSE STANDARD; PRT; 390 AA.
 AC O08970;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tuftelin.
 GN TUFT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.
 RC STRAIN=Swiss Webster; TISSUE=Tooth;
 RX MEDLINE=99053519; PubMed=9839784;
 RA MacDougall M., Simmons D., Dadds A., Knight C., Luan X.,
 RA Zeichner-David M., Zhang C., Ryu O.H., Qian Q., Qian Q., Simmer J.P., Hu C.-C.;
 RT "Cloning, characterization, and tissue expression pattern of mouse
 RT tuftelin cDNA".
 RL J. Dent. Res. 77:1970-1978(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=21590372; PubMed=11731143;
 RA Mao Z., Shay B., Hekmati M., Fermon E., Taylor A., Dafni L.,
 RA Heikinheimo K., Lustmann J., Fisher L.W., Young M.F., Deutsch D.;
 RT "The human tuftelin gene: cloning and characterization".
 RL Gene 279:181-196(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lochellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fabey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 7-324 FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC STRAIN=Swiss Webster;
 RX MEDLINE=97228909; PubMed=9074935;
 RA Zeichner-David M., Vo H., Nan H., Diekwisch T., Berman B.,
 RA Thiemann F., Alcocer M.D., Hsu P., Wang T., Eyna J., Caton J.,
 RA Slavkin H.C., MacDougall M.;

RT "Timing of the expression of enamel gene products during mouse tooth development.";
 RL Int. J. Dev. Biol. 41:27-38(1997).
 RN [5].
 RP INTERACTION WITH TFP11.
 RC STRAIN=Swiss Webster; TISSUE=Tooth;
 RX MEDLINE=20357353; PubMed=10806191;
 RA Paine C.T., Paine M.L., Luo W., Okamoto C.T., Lyngstadaas S.P.,
 RA Snead M.L.;
 RT "A tuftelin-interacting protein (TFP39) localizes to the apical
 RT secretory pole of mouse ameloblasts.";
 RL J. Biol. Chem. 275:22284-22292(2000).
 CC -!- FUNCTION: Involved in the mineralization and structural
 CC organization of enamel.
 CC -!- SUBUNIT: Interacts with TFP11. May form oligomers.
 CC -!- SUBCELLULAR LOCATION: Secreted at a very early stage of enamel
 CC formation, concentrated at the dentin-enamel junction and tightly
 CC bound to the surface of the growing crystallites (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O08970-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O08970-2; Sequence=VSP_006687;
 CC Name=3;
 CC IsoId=O08970-3; Sequence=VSP_006688;
 CC -!- TISSUE SPECIFICITY: Ameloblasts, and also nonodontogenic tissues
 CC including kidney, lung, liver and testis.
 CC -!- DEVELOPMENTAL STAGE: Expressed in tooth from E13, the bud stage.
 CC Continues to be expressed even when thick enamel is formed.
 CC -!- SIMILARITY: Belongs to the tuftelin family.
 CC
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 CC
 CC EMBL; AF047704; AAC04577.1; -;
 CC EMBL; BC019213; AAH19213.1; -;
 CC EMBL; AF002860; AAB60891.1; -;
 CC MSG; MGI:109572; Tuft1.
 CC GO; GO:0005576; C:extracellular; ISS.
 CC GO; GO:0030345; F:structural constituent of tooth enamel; ISS.
 CC GO; GO:0030282; P:bone mineralization; ISS.
 CC GO; GO:0042476; P:odontogenesis; ISS.
 CC Biomineralization; Coiled coil; Alternative splicing.
 CC DOMAIN 88 126 COILED COIL (POTENTIAL).
 CC DOMAIN 163 352 COILED COIL (POTENTIAL).
 CC FT VARSPLIC 21 45 Missing (in isoform 2 and isoform 3).
 CC FT VARSPLIC 96 356 /FTID=VSP_006687.
 CC FT VARSPLIC Missing (in isoform 3).
 CC FT /FTID=VSP_006688.
 CC SEQUENCE 390 AA; 44576 MW; 968FA7BBE95DFEC1 CRC64;
 CC
 CC Query Match 90.0%; Score 27; DB 1; Length 390;
 CC Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 EMQRR 6
 CC 230 EELQRR 235
 CC
 CC Db
 CC
 CC RESULT 11
 CC PURB PYRAB STANDARD; PRT; 450 AA.
 CC AC Q9UZ99;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinaae) (ASL).
 GN PURB OR PYRAB12550 OR PAB0829.
 OS Pyrococcus abyssi.
 OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 CC NCBI_TaxID=29292;
 CC [1]_TaxID=29292;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=GES / Orsay;
 RX MEDLINE=22511545; PubMed=12622808;
 RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
 RA Pech O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
 RA Van der Oost J., Weissenbach J., Zivanovic Y., Porterre P.;
 RT "An integrated analysis of the genome of the hyperthermophilic
 RT archaeon Pyrococcus abyssi.";
 RL Mol. Microbiol. 47:1495-1512(2003).
 CC -!- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxyethyl)AMP = fumarate + AMP.
 CC -!- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-
 CC ribosyl)imidazole-4-carboxamide]succinate = fumarate + 5-amino-1-
 CC (5-phospho-D-ribosyl)imidazole-4-carboxamide.
 CC -!- PATHWAY: De novo purine biosynthesis; eighth step.
 CC -!- SIMILARITY: Belongs to the lyase I family. Adenylosuccinate lyase
 CC subfamily.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AJ248287; CAB50160.1; -;
 CC PIR; C75033; C75033.
 CC HSP; Q9X010; IC3C.
 CC InterPro; IPR000362; Fumarate lyase.
 CC InterPro; IPR008948; L-Aspartase-like.
 CC InterPro; IPR004769; Pur lyase.
 CC Pfam; PF00206; Lyase I; 1.
 CC PRINTS; PR00149; FUMARATELYASE.
 CC TIGRfam; TIGR00928; purB; 1.
 CC PROSITE; PS00163; FUMARATE LYASES; 1.
 CC KX Purine biosynthesis; Lyase; Complete proteome.
 CC FT ACT SITE 76 76 ACID (BY SIMILARITY).
 CC FT ACT SITE 149 149 BASE (BY SIMILARITY).
 CC SEQUENCE 450 AA; 51455 MW; 82A3C0131455CDED CRC64;
 CC
 CC Query Match 90.0%; Score 27; DB 1; Length 450;
 CC Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 EMQRR 6
 CC 443 EEMERR 448
 CC
 CC Db
 CC
 CC RESULT 12
 CC PURB PYRHO STANDARD; PRT; 450 AA.
 CC AC O58582;
 CC DT 15-JUL-1999 (Rel. 38, Created)
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinaae) (ASL).
 GN PURB OR PH0852
 OS Pyrococcus horikoshii.
 OS Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 CC NCBI_TaxID=53953;
 CC [1]_TaxID=53953;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;

RA Kavarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ooura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku I.,
 RA Funahashi I., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.,
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -!- CATALYTIC ACTIVITY: N(6)-(1,2-dicarboxylethyl)AMP = fumarate + AMP.
 CC -!- CATALYTIC ACTIVITY: (S)-2-[5-amino-1-(5-phospho-D-
 ribosyl)imidazole-4-carboxamide]succinate = fumarate + 5-amino-1-
 (5-phospho-D-riboseyl)imidazole-4-carboxamide.
 CC -!- PATHWAY: De novo purine biosynthesis; eighth step.
 CC -!- SIMILARITY: Belongs to the lyase 1 family. Adenylosuccinate lyase
 subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AP000003; BAA29946.1; .
 DR PIR; H71135; H71135.
 DR HSSP; Q9X010; IC3C.
 DR InterPro; IPR000362; Fumarate_lyase.
 DR InterPro; IPR008948; L-Asparaginase-like.
 DR InterPro; IPR004769; Pur_lyase.
 DR Pfam; PF00206; Lyase 1; 1.
 DR PRINTS; PR00149; FUMRATELYASE.
 DR TIGRFAMs; TIGR00928; purB; 1.
 DR PROSITE; PS00163; FUMARATE_LYASES; 1.
 KW Purine biosynthesis; Lyase; Complete proteome.
 FT ACT SITE 76 76 ACID (BY SIMILARITY).
 FT ACT SITE 149 149 BASE (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 51644 MW; A700A652ADB822BC CRC64;
 Query Match 90.0%; Score 27; DB 1; Length 450;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 DB 443 EEMERR 448
 RESULT 13
 ID GATB TREPA STANDARD; PRT; 509 AA.
 AC 083984;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
 DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
 GN GATB OR TP1021
 OS Treponema pallidum.
 CC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=965876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
 RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;

RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RL Science 281:375-388(1998).
 CC -!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
 CC or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
 CC tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
 CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
 CC takes place in the presence of glutamine and ATP through an
 CC activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
 CC similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
 CC + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
 CC -!- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine = ADP
 CC + phosphate + L-asparaginyl-tRNA(Asn) + L-glutamate.
 CC -!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
 CC -!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
 CC -----
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 CC -----
 DR EMBL; AE001269; AAC65971.1; .
 DR PIR; A71254; A71254.
 DR TIGR; TP1021; .
 DR HAMAP; MF_00121; -. 1.
 DR InterPro; IPR004413; GatB.
 DR InterPro; IPR006107; GatB cent.
 DR InterPro; IPR006075; GatB N.
 DR InterPro; IPR003789; GatB_Yqey.
 DR Pfam; PF01162; GatB; 1.
 DR Pfam; PF02934; GatB N; 1.
 DR Pfam; PF02637; GatB_Yqey; 1.
 DR TIGRFAMs; TIGR00133; gatB; 1.
 DR PROSITE; PS01234; GATB; 1.
 KW Protein biosynthesis; Ligase; Complete proteome.
 SQ SEQUENCE 509 AA; 56865 MW; C28B9012236BF52 CRC64;
 Query Match 90.0%; Score 27; DB 1; Length 509;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 DB 272 EEMQRR 277
 RESULT 14
 ID ESR2 ONCMY STANDARD; PRT; 568 AA.
 AC P57782;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Estrogen receptor beta (ER-beta).
 GN ESR2 OR NR3A2.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RC SEQUENCE FROM N.A.
 RA Haug M., Ackermann G., Fent K.;
 RT "Molecular cloning of an estrogen receptor beta subtype from rainbow
 RT trout.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: BINDS ESTROGENS WITH AN AFFINITY SIMILAR TO THAT OF
 CC ER-ALPHA, AND ACTIVATES EXPRESSION OF REPORTER GENES CONTAINING
 CC ESTROGEN RESPONSE ELEMENTS (ERE) IN AN ESTROGEN-DEPENDENT MANNER.

```
CC -!- SUBUNIT: BINDS DNA AS A HOMODIMER. CAN FORM A HETERODIMER WITH ER-  
CC ALPHA (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DOMAIN: Composed of three domains: a modulating N-terminal domain,  
CC a DNA-binding domain and a C-terminal steroid-binding domain.  
CC -!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR3  
CC subfamily.  
CC -----  
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CC -----  
CC EMBL; AJ289983; CAC06714.1; -.  
CC HSP; P03372; 1ERR.  
CC InterPro; IPR000536; Hormone_rec_lig.  
CC InterPro; IPR001723; Steroid_receptor.  
CC InterPro; IPR008946; Str_ncl_receptor.  
CC InterPro; IPR001628; Znfc4steroid.  
CC Pfam; PF00104; hormone_rec; 1.  
CC Pfam; PF00105; zf-C4; 1.  
CC PRINTS; PR00398; STERDORMONER.  
CC PRINTS; PR00047; STROIDFINGER.  
CC ProDom; PD000035; Znfc4steroid; 1.  
CC SMART; SM00430; HOL1; 1.  
CC SMART; SM00399; Znfc4; 1.  
CC PROSITE; PS00031; NUCLEAR RECEPTOR; 1.  
CC Receptor; Transcription regulation; DNA-binding; Nuclear protein;  
CC Zinc-finger; Steroid-binding.  
CC DOMAIN 1 177 MODULATING  
CC DNAS BIND 178 243 NUCLEAR RECEPTOR-TYPE.  
CC ZN_FING 178 198 C4-TYPE.  
CC ZN_FING 214 238 C4-TYPE.  
CC DOMAIN 244 568 STEROID-BINDING.  
CC SEQUENCE 568 AA; 63813 MW; F7A7BD7B32C2804 CRC64;  
Query Match 30.0%; Score 27; DB 1; Length 568;  
Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEMQRR 6  
Db 456 EELQRR 461  
RESULT 15  
ID ILVD CORGL STANDARD; PRT; 613 AA.  
AC Q8NQZ9; Q9EW73;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).  
GN ILVD OR CGL1268.  
OS Corynebacterium glutamicum (Brevibacterium flavum).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI_TaxID=1718;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RA Ondrejko A., Eggeling L., Sahn H.;  
RT "Cloning and molecular analysis of the ilvd gene of Corynebacterium  
RT glutamicum."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RA Nakagawa S.;  
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
```

```
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-  
CC oxobutanoate + H(2)O.  
CC -!- COFACTOR: Binds 1 4Fe-4S cluster (Potential).  
CC -!- PATHWAY: Valine and isoleucine biosynthesis; fourth step.  
CC -!- SIMILARITY: Belongs to the ilvd / edd family.  
CC -----  
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CC -----  
CC EMBL; AJ012293; CAB57218.1; -.  
CC EMBL; AP005278; BAB98661.1; -.  
CC HAMAP; MF 00012; -. 1.  
CC InterPro; IPR004404; ILVD.  
CC InterPro; IPR000581; ILVD_EDD_family.  
CC Pfam; PF00920; ILVD_EDD; 1.  
CC ProDom; PD002691; ILVD_EDD_family; 2.  
CC TIGRFAMs; TIGR00110; ilvd; 1.  
CC PROSITE; PS00886; ILVD_EDD 1; 1.  
CC PROSITE; PS00887; ILVD_EDD 2; 1.  
CC Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;  
CC 4Fe-4S; Complete proteome.  
CC METAL 122 122 IRON-SULFUR (4FE-4S) (POTENTIAL).  
CC METAL 197 197 IRON-SULFUR (4FE-4S) (POTENTIAL).  
CC CONFLICT 78 78 MISSING (IN REF. 1).  
CC CONFLICT 157 158 DG -> ER (IN REF. 1).  
CC CONFLICT 188 188 A -> R (IN REF. 1).  
CC CONFLICT 332 332 G -> R (IN REF. 1).  
CC SEQUENCE 613 AA; 64674 MW; B422D52E6ACDB950 CRC64;  
Query Match 90.0%; Score 27; DB 1; Length 613;  
Best Local Similarity 83.3%; Pred. No. 2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EEMQRR 6  
Db 565 EELQRR 570  
Search completed: March 4, 2004, 08:25:55  
Job time : 7.63158 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:20 ; Search time 17.3684 Seconds
(without alignments)
72.944 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues 809742
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
6: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubaa/US09_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	206	10	US-09-942-024-2
2	30	100.0	206	10	US-09-942-024-7
3	30	100.0	206	10	US-09-942-024-12
4	30	100.0	206	10	US-09-942-024-12
5	30	100.0	206	10	US-09-942-098-7
6	30	100.0	206	10	US-09-942-098-12
7	30	100.0	249	10	US-09-942-024-16
8	30	100.0	249	10	US-09-942-098-16
9	27	90.0	35	13	US-10-029-217A-21
10	27	90.0	82	14	US-10-082-828A-255
11	27	90.0	214	9	US-09-925-300-1287
12	27	90.0	240	14	US-10-029-386-33812
13	27	90.0	245	9	US-09-925-299-791
14	27	90.0	245	10	US-09-925-299-791
15	27	90.0	345	14	US-10-156-761-10629

16	27	90.0	389	14	US-10-106-698-4653	Sequence 4653, Ap
17	27	90.0	435	15	US-10-369-493-13783	Sequence 13783, A
18	27	90.0	450	15	US-10-369-493-1266	Sequence 1266, Ap
19	27	90.0	450	15	US-10-369-493-20332	Sequence 20332, A
20	27	90.0	450	15	US-10-369-493-21647	Sequence 21647, A
21	27	90.0	510	14	US-10-128-714-3191	Sequence 3191, Ap
22	27	90.0	529	15	US-10-094-749-1678	Sequence 1678, Ap
23	27	90.0	613	9	US-09-738-626-4899	Sequence 4899, Ap
24	27	90.0	622	15	US-10-369-493-1366	Sequence 1366, Ap
25	27	90.0	632	14	US-10-128-714-8191	Sequence 8191, Ap
26	27	90.0	645	9	US-09-815-242-5823	Sequence 5823, Ap
27	27	90.0	727	9	US-09-801-368-296	Sequence 296, Ap
28	27	90.0	880	10	US-09-893-519A-36	Sequence 36, Appl
29	27	90.0	961	15	US-10-231-913-102	Sequence 102, Appl
30	27	90.0	1111	9	US-09-815-242-12955	Sequence 12955, A
31	27	90.0	1328	15	US-10-369-493-18867	Sequence 18867, A
32	27	90.0	1328	15	US-10-369-493-20000	Sequence 20000, A
33	27	90.0	2133	14	US-10-187-319-37	Sequence 37, Appl
34	27	90.0	2133	14	US-10-131-510A-37	Sequence 37, Appl
35	26	86.7	120	10	US-09-809-920-6	Sequence 6, Appli
36	26	86.7	265	15	US-10-369-493-7827	Sequence 7827, Ap
37	26	86.7	305	14	US-10-128-714-3145	Sequence 3145, Ap
38	26	86.7	315	14	US-10-128-714-8145	Sequence 8145, Ap
39	26	86.7	370	15	US-10-259-194A-44	Sequence 44, Appl
40	26	86.7	512	15	US-10-259-194A-224	Sequence 224, Appl
41	26	86.7	549	13	US-10-044-205A-14	Sequence 14, Appl
42	26	86.7	557	13	US-10-044-205A-13	Sequence 13, Appl
43	26	86.7	645	9	US-09-764-868-625	Sequence 625, App
44	26	86.7	663	14	US-10-102-806-654	Sequence 654, App
45	26	86.7	672	15	US-10-094-749-1885	Sequence 1885, Ap

ALIGNMENTS

RESULT 1
US-09-942-024-2
; Sequence 2, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AP 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-2

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 EEMQRR 6
Db 12 EEMQRR 17
RESULT 2
US-09-942-024-7
; Sequence 7, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger

; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-024-7

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 3

US-09-942-024-12
; Sequence 12, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-12

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 4

US-09-942-098-2
; Sequence 2, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-2

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 5

US-09-942-098-7
; Sequence 7, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-942-098-7

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 6

US-09-942-098-12
; Sequence 12, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-12

Query Match 100.0%; Score 30; DB 10; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||||
DB 12 EEMQRR 17

RESULT 7

US-09-942-024-16
; Sequence 16, Application US/09942024
; Publication No. US20030143650A1

LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE

; LOCATION: (193)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (203)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (207)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (210)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (211)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1287

Query Match 90.0%; Score 27; DB 9; Length 214;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 65 BELQRR 70
||:||||

RESULT 12
US-10-029-386-33812
; Sequence 33812, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David K.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AECOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33812
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALL36001.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.37
; OTHER INFORMATION: SWISSPROT HIT: Q9JL04, EVALUE 1.20e+00
US-10-029-386-33812

Query Match 90.0%; Score 27; DB 14; Length 240;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 229 EEMQRR 234
|||:|

RESULT 13
US-09-925-299-791
; Sequence 791, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 791
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-791

Query Match 90.0%; Score 27; DB 9; Length 245;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 136 BELQRR 141
||:||||

RESULT 14
US-09-925-299-791
; Sequence 791, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 791
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-791

Query Match 90.0%; Score 27; DB 10; Length 245;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 136 BELQRR 141
||:||||

RESULT 15
US-10-156-761-10629
; Sequence 10629, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10629
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis

US-10-156-761-10629

Query Match 90.0%; Score 27; DB 14; Length 345;
Best Local Similarity 83.3%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||:
Db 214 EEMERR 219

Search completed: March 4, 2004, 08:30:59
Job time : 17.3684 secs

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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:26:00 ; Search time 10.1053 Seconds
(without alignments)
30.653 Million cell updates/sec

Title: US-10-030-485A-2

Perfect score: 30

Sequence: 1 BEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pap.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	68	4	US-09-621-976-7614
2	30	100.0	286	1	US-08-393-985-18
3	30	100.0	206	3	US-08-819-286-1
4	27	90.0	200	4	US-09-252-991A-23347
5	27	90.0	231	4	US-09-252-991A-27366
6	27	90.0	314	4	US-09-543-681A-5695
7	27	90.0	375	1	US-07-803-622E-7
8	27	90.0	375	1	US-07-803-622E-9
9	27	90.0	534	4	US-09-107-532A-6549
10	27	90.0	612	3	US-09-318-794A-5
11	27	90.0	739	1	US-07-863-622E-2
12	27	90.0	868	1	US-07-864-004B-6
13	27	90.0	868	1	US-08-251-937A-6
14	27	90.0	868	1	US-08-212-133A-3
15	27	90.0	914	4	US-09-437-054A-8
16	27	90.0	1090	5	PCT-US93-03275-6
17	27	90.0	1115	3	US-09-324-867-5
18	27	90.0	2133	2	US-08-670-707A-37
19	27	90.0	2133	3	US-09-037-601-37
20	27	90.0	2133	4	US-09-315-179-37
21	27	90.0	2133	4	US-09-523-656-30
22	26	86.7	253	4	US-09-252-991A-31497
23	26	86.7	362	4	US-09-107-532A-7093
24	26	86.7	363	4	US-09-252-991A-32850
25	26	86.7	496	4	US-09-252-991A-20207
26	26	86.7	496	4	US-09-540-236-3821
27	26	86.7	728	3	US-08-915-337-2

28	26	86.7	1251	4	US-09-698-286A-9	Sequence 9, Appli
29	26	86.7	1375	4	US-09-722-139-2	Sequence 2, Appli
30	26	86.7	1375	4	US-09-721-832-2	Sequence 2, Appli
31	26	86.7	1375	4	US-09-721-689-2	Sequence 2, Appli
32	25	83.3	98	4	US-09-489-039A-7345	Sequence 7345, Ap
33	25	83.3	108	4	US-09-328-352-5930	Sequence 5930, Ap
34	25	83.3	203	4	US-09-489-039A-7593	Sequence 7593, Ap
35	25	83.3	235	2	US-09-141-135-2	Sequence 2, Appli
36	25	83.3	235	4	US-09-533-029-98	Sequence 98, Appli
37	25	83.3	255	4	US-09-364-230-34	Sequence 34, Appli
38	25	83.3	277	4	US-09-489-039A-7505	Sequence 7505, Ap
39	25	83.3	341	4	US-09-252-991A-27327	Sequence 27327, A
40	25	83.3	346	3	US-09-049-672A-28	Sequence 28, Appli
41	25	83.3	378	4	US-09-107-532A-6500	Sequence 6500, Ap
42	25	83.3	392	4	US-09-600-099-6	Sequence 6, Appli
43	25	83.3	415	4	US-09-252-991A-30511	Sequence 30511, A
44	25	83.3	452	4	US-09-277-262-8	Sequence 8, Appli
45	25	83.3	471	3	US-08-866-928B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-621-976-7614
; Sequence 7614, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 7614
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7614

Query Match 100.0%; Score 30; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BEMQRR 6
DB 12 BEMQRR 17

RESULT 2
US-08-393-985-18
; Sequence 18, Application US/08393985
; Patent No. 5693476
; GENERAL INFORMATION:
; APPLICANT: Scheller, Richard H.
; TITLE OF INVENTION: Methods and Compositions for Modulation
; TITLE OF INVENTION: of Vesicular Release
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,985
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8600-0152
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-985-18

Query Match 100.0%; Score 30; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 3
US-08-819-286-1
; Sequence 1, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-819-286-1

Query Match 100.0%; Score 30; DB 3; Length 206;

Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
|||
Db 12 EEMQRR 17

RESULT 4
US-09-252-991A-23347
; Sequence 23347, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23347
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23347

Query Match 90.0%; Score 27; DB 4; Length 200;
Best Local Similarity 83.3%; Pred. No. 2,4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
|||
Db 86 EELQRR 91

RESULT 5
US-09-252-991A-27366
; Sequence 27366, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27366
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27366

Query Match 90.0%; Score 27; DB 4; Length 231;
Best Local Similarity 83.3%; Pred. No. 2,7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEMQRR 6
|||
Db 203 EELQRR 208

RESULT 6
US-09-543-681A-5695
; Sequence 5695, Application US/09543681A

Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5695
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-5695

Query Match 90.0%; Score 27; DB 4; Length 314;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
DB 135 EELQR 140

RESULT 7
US-07-803-622E-7
; Sequence 7, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-803-622E-7

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
DB 135 EELQR 140

RESULT 8
US-07-803-622E-9
; Sequence 9, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY(A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-803-622E-9

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
DB 56 EELQR 61

RESULT 9
US-09-107-532A-6549
; Sequence 6549, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

Query Match 90.0%; Score 27; DB 1; Length 375;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
DB 56 EELQR 61


```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Atinello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6549:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...534
; SEQUENCE DESCRIPTION: SEQ ID NO: 6549:
US-09-107-532A-6549

```

```

Query Match          90.0%; Score 27; DB 4; Length 534;
Best Local Similarity 83.3%; Pred. No. 5.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EEMQRR 6
DB      39 EEMERR 44

```

```

RESULT 10
US-09-318-794A-5
; Sequence 5, Application US/09318794A
; Patent No. 6177264
; GENERAL INFORMATION:
; APPLICANT: DEGUSSA AKTIENGESSELLSCHAFT
; TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
; FILE OF INVENTION: ACID USING CORNEFORM BACTERIA
; FILE REFERENCE: eggeling
; CURRENT APPLICATION NUMBER: US/09/318,794A
; CURRENT FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: DE 198 55 312.9
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-318-794A-5

```

```

Query Match          90.0%; Score 27; DB 3; Length 612;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EEMQRR 6
DB      564 EELQRR 569

```

```

RESULT 11
US-07-803-622E-2
; Sequence 2, Application US/07803622E
; Patent No. 5525497
; GENERAL INFORMATION:
; APPLICANT: Keller, Walter
; APPLICANT: Lingner, Joachim
; APPLICANT: Martin, Georges
; APPLICANT: Wahle, Elmar
; TITLE OF INVENTION: RECOMBINANT POLY (A) POLYMERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/803,622E
; FILING DATE: 27-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 195/296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 739 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-803-622E-2

```

```

Query Match          90.0%; Score 27; DB 1; Length 739;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EEMQRR 6
DB      56 EELQRR 61

```

```

RESULT 12
US-07-864-004B-6
; Sequence 6, Application US/07864004B
; Patent No. 5364771
; GENERAL INFORMATION:
; APPLICANT: Iollar, John S.
; APPLICANT: Runge, Marshall S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA: US/07/864,004B
;; FILING DATE: 07 APRIL 1992
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Pabst, Patrea L.
;; REGISTRATION NUMBER: 31,284
;; REFERENCE/DOCKET NUMBER: EMU106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 404-815-6508
;; TELEFAX: 404-815-6555
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 868 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Porcine
US-07-864-004B-6

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 418 EEMERR 423

RESULT 13
US-08-251-937A-6
; Sequence 6, Application US/08251937A
; Patent No. 5583209
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30309
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/251,937A
; FILING DATE: 31-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pratt, John S.
; REGISTRATION NUMBER: 29,476
; REFERENCE/DOCKET NUMBER: EMU106DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-815-6367
; TELEFAX: 404-815-6555
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Porcine
US-08-251-937A-6

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 418 EEMERR 423

RESULT 14
US-08-212-133A-3
; Sequence 3, Application US/08212133A
; Patent No. 5663060
; GENERAL INFORMATION:
; APPLICANT: Lollar, John S.
; TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 100 Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: US
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,133A
; FILING DATE: March 11, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,004
; FILING DATE: 07-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: EMU/76677
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-572-6508
; TELEFAX: 404-572-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 868 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Porcine
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..868
; OTHER INFORMATION:
; OTHER INFORMATION: sequence of the B and part of the A2 domains of
; OTHER INFORMATION: porcine factor VIII."

US-08-212-133A-3

Query Match 90.0%; Score 27; DB 1; Length 868;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQR 6
|||:
Db 418 EEMER 423

RESULT 15

US-09-437-054A-8
; Sequence 8, Application US/09437054A
; Patent No. 6316698
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Alpha-Glucosidase II Homologs
; FILE REFERENCE: BB1273 US NA
; CURRENT APPLICATION NUMBER: US/09/437,054A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/107,909
; PRIOR FILING DATE: 1998-No. 6316698ember-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Glycine max
US-09-437-054A-8

Query Match 90.0%; Score 27; DB 4; Length 914;
Best Local Similarity 83.3%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQR 6
|||:
Db 413 EEMQR 418

Search completed: March 4, 2004, 08:31:45
Job time : 11.1053 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 4, 2004, 08:25:19 ; Search time 31.8947 Seconds
(without alignments)
53.153 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep 29Jan04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	6	4	AAB15582 Human SNA
2	30	100.0	13	4	AAB15583 Human SNA
3	30	100.0	64	3	AG00764 Human sec
4	30	100.0	82	4	AAB15581 Human SNA
5	30	100.0	93	6	ABU43453 Protein e
6	30	100.0	106	3	AG03825 Human sec
7	30	100.0	106	3	AG03826 Human sec
8	30	100.0	198	4	AAU00255 Synapto
9	30	100.0	199	4	AAU00263 Synapto
10	30	100.0	200	4	AAU00264 Synapto
11	30	100.0	201	4	AAU02637 Synapto
12	30	100.0	202	4	AAU00265 Synapto
13	30	100.0	203	4	AAU02636 Synapto
14	30	100.0	206	2	AAW30103 Synapto
15	30	100.0	206	2	AAW43426 Mouse syn
16	30	100.0	206	2	AAW79198 Mouse SNA
17	30	100.0	206	4	AAU00256 Synapto
18	30	100.0	206	4	AAU00261 Synapto
19	30	100.0	206	4	AAU00246 Synapto
20	30	100.0	206	4	AAU00253 SNARE hom
21	30	100.0	206	4	AAU02171 Synapto
22	30	100.0	206	4	AAU00266 Synapto
23	30	100.0	206	4	AAU02640 Synapto
24	30	100.0	206	4	AAU00258 Synapto
25	30	100.0	206	4	AAU00262 Synapto

26	30	100.0	206	4	AAU00259 Synapto
27	30	100.0	206	4	AAU00252 SNARE hom
28	30	100.0	206	4	AAU00260 Synapto
29	30	100.0	206	4	AAU02638 Synapto
30	30	100.0	206	4	AAU002639 Synapto
31	30	100.0	206	4	AAU00257 Synapto
32	30	100.0	206	6	AAE36662 Human SNA
33	30	100.0	206	6	AAE36667 Rat VAMP-
34	30	100.0	206	7	ADE54280 Rat Prote
35	30	100.0	206	7	ADE54288 Rat Prote
36	30	100.0	206	7	ADE54276 Rat Prote
37	30	100.0	206	7	ADE54290 Human Pro
38	30	100.0	206	7	ADE54282 Rat Prote
39	30	100.0	206	7	ADE54274 Rat Prote
40	30	100.0	206	7	ADE54286 Human Pro
41	30	100.0	206	7	ADE54284 Rat Prote
42	30	100.0	206	7	ADE54272 Rat Prote
43	30	100.0	206	7	ADE54278 Rat Prote
44	30	100.0	537	4	ABB59734 Drosophil
45	27	90.0	35	5	ABG70819 Mouse myo

ALIGNMENTS

RESULT 1
AAB15582
ID AAB15582 standard; peptide; 6 AA.

XX AC AAB15582;
XX DT 02-MAR-2001 (first entry)
XX DE Human SNAP-25 N-terminal peptide #2.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
XX KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
XX KW neurodegenerative disorder.

XX OS Homo sapiens.
XX PN WO200064932-A1.
XX PD 02-NOV-2000.
XX PF 18-FEB-2000; 2000WO-ES000058.
XX PR 23-APR-1999; 99ES-00000844.
(LIPO-) LIPOTEC SA.

XX PA Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;
XX PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;
XX PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;
XX PI Perez Paya E;
XX DR WPI; 2001-007091/01.

XX PT New peptides containing amino acid sequences from known proteins for
XX PT treatment of neurological disorders.
XX PS Claim 9; Page 32; 40pp; Spanish.

XX CC The invention relates to new peptides comprising 3-30 contiguous amino
XX CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
XX CC protein 25). The peptides AAB15581-B15586 represent examples of the
XX CC peptides of the invention. The peptides have neuronal exocytosis
XX CC inhibitory activity and are used for treatment of facial wrinkles and
XX CC asymmetry and pathological neuronal exocytosis-mediated pathological
XX CC disorders and alterations manifested e.g. by spasms and neurological and
XX CC neurodegenerative disorders
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 30; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
Db 1 EEMQRR 6

RESULT 2

AAB15583
ID AAB15583 standard; peptide; 13 AA.

XX AC AAB15583;

XX DT 02-MAR-2001 (first entry)

XX DE Human SNAP-25 N-terminal peptide #3.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;
KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;
KW neurodegenerative disorder.

XX OS Homo sapiens.

XX PN WO200064932-A1.

XX PD 02-NOV-2000.

XX PF 18-FEB-2000; 2000WO-ES000058.

XX PR 23-APR-1999; 99ES-00000844.

XX PA (LIPO-) LIPOTEC SA.

XX PI Blanes Mira MC, Llobregat Hernandez MM, Gil Tebar AI;

XX PI Fernandez Ballester GJ, Planell Cases RM, Ferrer Montiel AV;

XX PI Viniegra Bover S, Gutierrez Perez LM, Carbonell Castell T;

XX PI Perez Paya E;

XX DR WPI; 2001-007091/01.

XX PT New peptides containing amino acid sequences from known proteins for
PT treatment of neurological disorders.

XX PS Claim 9; Page 32; 40pp; Spanish.

XX CC The invention relates to new peptides comprising 3-30 contiguous amino
CC acids from the N-terminus of the protein SNAP-25 (synaptosomal-associated
CC protein 25). The peptides AAB15581-B15586 represent examples of the
CC peptides of the invention. The peptides have neuronal exocytosis
CC inhibitory activity and are used for treatment of facial wrinkles and
CC asymmetry and pathological neuronal exocytosis-mediated pathological
CC disorders and alterations manifested e.g. by spasms and neurological and
CC neurodegenerative disorders

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 30; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
Db 3 EEMQRR 8

RESULT 3

AAG00764

ID AAG00764 standard; protein; 64 AA.

XX AC AAG00764;

XX

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 4845.

XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.

XX OS Homo sapiens.

XX PN EP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX DR N-PSDB; AAC00770.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX PS Claim 13; SEQ ID NO 4845; 71pp + Sequence Listing; English.

XX CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or poly(A)⁺ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX SQ Sequence 64 AA;

Query Match 100.0%; Score 30; DB 3; Length 64;

Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
Db 12 EEMQRR 17

RESULT 4

AAB15581

ID AAB15581 standard; peptide; 82 AA.

XX AC AAB15581;

XX DT 02-MAR-2001 (first entry)

XX DE Human SNAP-25 N-terminal peptide #1.

XX KW Dermatological; neuroprotective; relaxant; neuronal exocytosis modulator;

XX KW SNAP-25; synaptosomal-associated protein 25; facial wrinkle; asymmetry;

XX KW neurodegenerative disorder.

XX OS Homo sapiens.

XX PN WO200064932-A1.

DR	N-PSDB; ACA47323.
XX	
PT	New antisense nucleic acids, useful for identifying proteins or screening
PT	for homologous nucleic acids required for cellular proliferation to
PT	isolate candidate molecules for rational drug discovery programs.
XX	
PS	Claim 25; SEQ ID NO 71377; 1766pp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising any one of
CC	the 6213 antisense sequences given in the specification where expression
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:
CC	(1) a vector comprising a promoter operably linked to the nucleic acid
CC	encoding a polypeptide whose expression is inhibited by the antisense
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC	polypeptide or its fragment whose expression is inhibited by the
CC	antisense nucleic acid; (4) an antibody capable of specifically binding
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC	proliferation or the activity of a gene in an operon required for
CC	proliferation; (7) identifying a compound that influences the activity of
CC	the gene product or that has an activity against a biological pathway
CC	required for proliferation, or that inhibits cellular proliferation; (8)
CC	identifying a gene required for cellular proliferation or the biological
CC	pathway in which a proliferation-required gene or its gene product lies
CC	or a gene on which the test compound that inhibits proliferation of an
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC	compound's activity; (11) a culture comprising strains in which the gene
CC	product is overexpressed or underexpressed; (12) determining the extent
CC	to which each of the strains is present in a culture or collection of
CC	strains; or (13) identifying the target of a compound that inhibits the
CC	proliferation of an organism. The antisense nucleic acids are useful for
CC	identifying proteins or screening for homologous nucleic acids required
CC	for cellular proliferation to isolate candidate molecules for rational
CC	drug discovery programs, or for screening homologous nucleic acids
CC	required for proliferation in cells other than <i>S. aureus</i> , <i>S. typhimurium</i> ,
CC	<i>K. pneumoniae</i> or <i>P. aeruginosa</i> . The present sequence is encoded by one of
CC	the target prokaryotic essential genes. Note: The sequence data for this
CC	patent did not form part of the printed specification, but was obtained
CC	in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 93 AA;
Query Match 100.0%; Score 30; DB 6; Length 93;	
Best Local Similarity 100.0%; Pred. No. 1e+02;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 EEMQRR 6
Db	24 EEMQRR 29
RESULT 6	
AAG03825	ID AAG03825 standard; protein; 106 AA.
XX	
AC	AAG03825;
XX	
DT	06-OCT-2000 (first entry)
XX	
DE	Human secreted protein, SEQ ID NO: 7906.
XX	
XW	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XW	gene therapy; chromosome mapping.
OS	Homo sapiens.
PN	EP1033401-A2.
PD	06-SEP-2000.
XX	
XX	21-FEB-2000; 2000EP-00200610.
PR	26-FEB-1999; 99US-0122487P.

XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC03831.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX PS Claim 13; SEQ ID NO 7906; 71pp + Sequence Listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ Sequence 106 AA;
 Query Match 100.0%; Score 30; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db |||||
 12 EEMQRR 17
 RESULT 7
 ID AAG03826
 XX AAG03826 standard; protein; 106 AA.
 AC AAG03826;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 7907.
 XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 XX KW gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN EP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX DR WPI; 2000-500381/45.
 XX DR N-PSDB; AAC03832.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX SQ

PS Claim 13; SEQ ID NO 7907; 71pp + Sequence Listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ Sequence 106 AA;
 Query Match 100.0%; Score 30; DB 3; Length 106;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db |||||
 12 EEMQRR 17
 RESULT 8
 ID AAU00255
 XX AAU00255 standard; protein; 198 AA.
 AC AAU00255;
 XX DT 12-SEP-2001 (first entry)
 XX DE Synaptosomal-associated protein, SNAP25, C-terminal deletion 1-198.
 XX KW SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.
 XX OS Mus sp.
 XX OS Synthetic.
 XX PN WO200118038-A2.
 XX PD 15-MAR-2001.
 XX PF 18-AUG-2000; 2000WO-GB003196.
 XX PR 20-AUG-1999; 99US-0149993P.
 XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, C-terminal deletion 1-198, used in a new
 CC method of treating a patient suffering from poisoning or at risk of
 CC poisoning by a clostridial toxin, comprising supplying a SNARE (soluble
 CC (N-ethylmaleimide-sensitive fusion protein)-attachment protein receptor)
 CC to a cell of the patient, where the SNARE is resistant to proteolysis by
 CC the toxin (toxin-resistant SNARE) and/or is capable of inhibiting the

CC toxin (toxin-inhibitory SNARE). The protein can be used in a method of
 CC treating a patient in need of inhibition of SNARE-dependent exocytosis
 CC from a cell capable of performing SNARE-dependent exocytosis, comprises
 CC supplying a fragment, variant, fusion or derivative of a SNARE or an
 CC inhibitory SNARE to the cell of the patient. The toxin resistant or toxin
 CC inhibitory SNARE or a recombinant polynucleotide encoding the SNARE is
 CC useful in the manufacture of a medicament for the treatment of a patient
 CC suffering from poisoning or at risk of poisoning by clostridial toxin,
 CC e.g. from botulism or tetanus. The fragment, variant, fusion or
 CC derivative of a SNARE or of an inhibitory SNARE, or a recombinant
 CC polynucleotide encoding either of these SNARE polypeptides are useful in
 CC the manufacture of medicament for the treatment of a patient in need of
 CC inhibition of SNARE-dependent exocytosis from a cell capable of
 CC performing SNARE-dependent exocytosis. The method of treatment is
 CC relatively fast, thus alleviating the symptoms when most severe and
 CC taking the patient out of critical state. Note: The present sequence is
 CC not shown in the specification but is derived from the mouse SNAP-25
 CC sequence given in figure 8 (see AAU00246)

XX Sequence 198 AA;

Query Match 100.0%; Score 30; DB 4; Length 198;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

DB 12 EEMQRR 17

RESULT 9
 AAU00263
 ID AAU00263 standard; protein; 199 AA.

XX AAU00263;
 XX 12-SEP-2001 (first entry)
 XX Synaptosomal-associated protein, SNAP25, mutant 1-199 (R198T).
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Key Location/Qualifiers

FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.

XX Example 1; Page; 131pp; English.

CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-199 (R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding a
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)

XX Sequence 199 AA;

Query Match 100.0%; Score 30; DB 4; Length 199;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6

DB 12 EEMQRR 17

RESULT 10
 AAU00264
 ID AAU00264 standard; protein; 200 AA.

XX AAU00264;

XX 12-SEP-2001 (first entry)

XX Synaptosomal-associated protein, SNAP25, mutant 1-200 (R198T).

XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 198 /note= "Wild-type Arg substituted by Thr"

XX WO200118038-A2.

XX 15-MAR-2001.

XX 18-AUG-2000; 2000WO-GB003196.

XX 20-AUG-1999; 99US-0149993P.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

PI Dolly JO, O'sullivan GA, Mohammed N, Foran PG;

XX WPI; 2001-226739/23.

XX PT Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX PS Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-200(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX SQ Sequence 200 AA;

Query Match 100.0%; Score 30; DB 4; Length 200;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEMQRR 6
 |||||
 Db 12 EEMQRR 17

RESULT 11
 AAU02637
 ID AAU02637 standard; protein; 201 AA.
 AC AAU02637;
 DT 12-SEP-2001 (first entry)
 XX Synaptosomal-associated protein, SNAP25, mutant 1-201(R198T).
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT
 XX WO200118038-A2.
 XX 15-MAR-2001.
 XX 18-AUG-2000; 2000WO-GB003196.
 XX

PR 20-AUG-1999; 99US-0149993P.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX Dolly JO, O'sullivan GA, Mohammed N, Foran PG;
 XX WPI; 2001-226739/23.
 XX Treating a patient suffering from poisoning or at risk of poisoning by a
 PT clostridial toxin, e.g. botulism, comprises administering a toxin-
 PT resistant or toxin-inhibitory SNARE.
 XX Example 1; Page; 131pp; English.
 XX CC The sequence represents the amino acid sequence of synaptosomal-
 CC associated protein, SNAP25, mutant 1-201(R198T), used in a new method of
 CC treating a patient suffering from poisoning or at risk of poisoning by a
 CC clostridial toxin, comprising supplying a SNARE (soluble (N-
 CC ethylmaleimide-sensitive fusion protein)-attachment protein receptor) to
 CC a cell of the patient, where the SNARE is resistant to proteolysis by the
 CC toxin (toxin-resistant SNARE) and/or is capable of inhibiting the toxin
 CC (toxin-inhibitory SNARE). The protein can be used in a method of treating
 CC a patient in need of inhibition of SNARE-dependent exocytosis from a cell
 CC capable of performing SNARE-dependent exocytosis, comprises supplying a
 CC fragment, variant, fusion or derivative of a SNARE or an inhibitory SNARE
 CC to the cell of the patient. The toxin resistant or toxin inhibitory SNARE
 CC or a recombinant polynucleotide encoding the SNARE is useful in the
 CC manufacture of a medicament for the treatment of a patient suffering from
 CC poisoning or at risk of poisoning by clostridial toxin, e.g. from
 CC botulism or tetanus. The fragment, variant, fusion or derivative of a
 CC SNARE or of an inhibitory SNARE, or a recombinant polynucleotide encoding
 CC either of these SNARE polypeptides are useful in the manufacture of
 CC medicament for the treatment of a patient in need of inhibition of SNARE-
 CC dependent exocytosis from a cell capable of performing SNARE-dependent
 CC exocytosis. The method of treatment is relatively fast, thus alleviating
 CC the symptoms when most severe and taking the patient out of critical
 CC state. Note: The present sequence is not shown in the specification but
 CC is derived from the mouse SNAP-25 sequence given in figure 8 (see
 CC AAU00246)
 XX SQ Sequence 201 AA;

Query Match 100.0%; Score 30; DB 4; Length 201;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EEMQRR 6
 |||||
 Db 12 EEMQRR 17

RESULT 12
 AAU00265
 ID AAU00265 standard; protein; 202 AA.
 AC AAU00265;
 DT 12-SEP-2001 (first entry)
 XX Synaptosomal-associated protein, SNAP25, mutant 1-202(R198T).
 XX SNAP-25; poisoning; clostridial toxin; SNARE; toxin-resistant SNARE;
 KW toxin-inhibitory SNARE; botulism; tetanus; SNARE-dependent exocytosis;
 KW synaptosomal-associated protein; mouse; mutant; mutein;
 KW N-ethylmaleimide-sensitive fusion protein;
 KW soluble NSF-attachment protein receptor.

XX Mus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 PH Misc-difference 198 /note= "Wild-type Arg substituted by Thr"
 FT

DE Synaptosomal associated protein.
 XX Neurotransmitter secretion; inhibitor; neuronal cell; synaptic vesicle;
 KW excitation-secretory uncoupling peptide; catecholamine secretion;
 KW bovine chromaffin cell; Clostridium toxin; muscle spasticity reduction;
 KW synaptosomal associated protein; SNAP-25.
 XX
 OS Homo sapiens.
 PN WO9734620-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 18-MAR-1997; 97WO-US004393.
 XX
 PR 18-MAR-1996; 96US-0013599P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Montal M;
 XX
 DR WPI; 1997-479986/44.
 XX
 CC Excitation-secretory uncoupling peptide(s) for inhibiting
 PT neuro:transmitter release - used particularly for treating muscle
 PT spasticity, and for delivering drugs specifically to neural cells.
 XX
 PS Disclosure; Page 27-28; 61pp; English.
 XX
 CC This sequence represents the human 25 kD synaptosomal associated protein
 CC (SNAP-25), which is an inhibitor agent of the invention. The agents of
 CC the invention inhibit secretion of neurotransmitter from neuronal cells
 CC and is an excitation-secretory uncoupling peptide (I) of at least 20
 CC amino acids (aa) all of which correspond substantially to any one of
 CC AAW30097-W30102, or more generally any (I) that inhibits 50% of
 CC catecholamine secretion from bovine chromaffin cells at a concentration
 CC of 10 microm, especially 0.25 microm, or less. (I) are used, as a
 CC replacement for Clostridium toxin, to inhibit release of
 CC neurotransmitters from synaptic vesicles, specifically for reducing
 CC muscle spasticity. Also (I) may be labelled to allow in vivo imaging of
 CC intracellular distribution of (I). Compounds for delivering the drug to
 CC neural cells provided targeted drug delivery, e.g. of substance P to brain
 CC tumours for induction of apoptosis. Unlike the neurotoxins, (I) are not
 CC toxic or immunogenic and are more readily available. Their therapeutic
 CC effect lasts for several days or weeks, so lower doses or less frequent
 CC treatments are required
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 30; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 RESULT 15
 AAW43426
 ID AAW43426 standard; protein; 206 AA.
 XX
 AC AAW43426;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse synaptosomal-associated protein-25.
 XX
 KW Binding domain; mouse; syntaxin; synaptosomal-associated protein; CNS;
 KW neurotransmitter; presynaptic membrane; central nervous system; tumour;
 KW neurodegenerative disease; hormonal disorder; immunological disorder.
 XX
 OS Mus sp.

XX US5693476-A.
 XX
 PD 02-DEC-1997.
 XX
 PF 24-FEB-1995; 95US-00393985.
 XX
 PR 24-FEB-1995; 95US-00393985.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Scheller RH;
 XX
 DR WPI; 1998-031743/03.
 XX
 DR N-PSDB; AAV01554.
 XX
 PT Screening assay for modulators of syntaxin binding - using peptide
 PT comprising binding site of syntaxin, for identifying drugs useful for
 PT treating CNS disorders, neuro-degenerative diseases, etc.
 XX
 PS Disclosure; Col 67-72; 57pp; English.
 XX
 CC This amino acid sequence represents the mouse synaptosomal-associated
 CC protein of 25 kD (SNAP-25). The invention relates to a method for
 CC identifying a compound capable of affecting the binding of a syntaxin-
 CC binding protein (SBP), e.g. SNAP-25, alpha-SNAP, n-secl or VAMP, to
 CC syntaxin. The method comprises measuring the effect of the test compound
 CC on the extent of binding between the SBP and the SBP-binding site on
 CC syntaxin. The method can be used for identifying drugs capable of
 CC inhibiting or stimulating neurotransmitter release at the active zones of
 CC presynaptic membranes, which may be useful for treating CNS disorders,
 CC affective or psychotic disorders, neurodegenerative diseases, hormonal or
 CC immunological disorders or tumours
 XX
 SQ Sequence 206 AA;
 Query Match 100.0%; Score 30; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEMQRR 6
 Db 12 EEMQRR 17
 Search completed: March 4, 2004, 08:27:49
 Job time : 32.8947 secs

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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:04:11 ; Search time 35.5135 Seconds
(without alignments)
159.920 Million cell updates/sec

Title: US-10-030-485A-5

Perfect score: 89
Sequence: 1 RIMEKADSNKTRIDEANQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	89	100.0	124	13	Q93578 brachydanio
2	89	100.0	143	6	Q9GM34 macaca fasc
3	80	89.9	203	13	Q93579 brachydanio
4	80	89.9	206	13	Q8AXM2 xenopus lae
5	80	89.9	206	13	Q8AXM1 xenopus lae
6	70	78.7	204	13	Q8JIS7 xenopus lae
7	70	78.7	214	13	Q7ZVE4 brachydanio
8	65	73.0	212	5	Q8T3S4 loligo peal
9	59	66.3	210	11	Q35620 mus musculus
10	59	66.3	210	11	Q70377 rattus norv
11	59	66.3	210	11	Q09044 mus musculus
12	59	66.3	221	11	Q9D3I3 mus musculus
13	50	56.2	90	5	Q96578 leucophaea
14	50	56.2	125	5	O96576 leucophaea
15	50	56.2	207	5	O62414 caenorhabdi
16	48	53.9	1202	10	Q8LMQ4 oryza sativ

17	47	52.8	659	10	Q41074
18	46	51.7	240	2	Q9RGE7
19	45	50.6	1138	5	Q22276
20	44	49.4	191	17	Q8ZY72
21	44	49.4	212	5	O44419
22	44	49.4	212	5	O76338
23	44	49.4	220	5	Q869G6
24	44	49.4	584	2	Q9KH13
25	44	49.4	776	16	Q89QI8
26	44	49.4	1297	5	Q8IC22
27	43	48.3	395	4	Q96LN4
28	43	48.3	401	16	Q9PIU7
29	43	48.3	480	5	Q17621
30	43	48.3	623	4	Q8NCN6
31	43	48.3	1036	5	Q81950
32	42.5	47.8	524	3	Q9P8E5
33	42	47.2	86	15	P89733
34	42	47.2	173	16	Q45938
35	42	47.2	207	5	Q8IAE1
36	42	47.2	207	5	Q8IAE0
37	42	47.2	212	5	O01389
38	42	47.2	304	2	Q9K580
39	42	47.2	334	6	Q95JR9
40	42	47.2	403	16	O7WJ36
41	42	47.2	419	2	Q9ZFG6
42	42	47.2	447	2	Q9AGH6
43	42	47.2	551	6	Q95UV6
44	42	47.2	658	5	O76180
45	42	47.2	659	5	Q81866

ALIGNMENTS

RESULT 1
O93578 PRELIMINARY; PRT; 124 AA.
AC O93578
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Synaptosome-associated protein 25.1 (Fragment).
GN SNAP25A OR SNAP
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9057281; PubMed=9843147;
RA Risinger C., Salanek E., Soderberg C., Gates M., Postlethwait J.H.,
RA Larhammar D.;
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
RT comparison of paralogous linkage groups suggests loss of one locus in
RT the mammalian lineage".
RL J. Neurosci. Res. 54:563-573 (1998).
DR EMBL; AF091593; AAC64289.1; -.
DR ZFIN; ZDB-GENE-980526-468; snap25a.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T_SNARE.
DR Pfam; PF00835; SNAP-25_1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SMO0397; t_SNARE; 1.
DR PROSITE; PSS0192; T_SNARE; 1.
FT NON TER 1 -1
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBD33D958C CRC64;

Query Match 100.0%; Score 89; DB 13; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIMEKADSNKTRIDEANQ 18

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DR PFAM: PF05739; SNARE; 1.
DR SMART: SM00397; t_SNARE; 2.
DR PROSITE: PS50192; t_SNARE; 2.
SQ SEQUENCE 203 AA; 22647 MW; 93B7590DD0C93F38 CRC64;

Query Match 89.9%; Score 80; DB 13; Length 203;
Best Local Similarity 88.9%; Pred. No. 7.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 177 RIMWADSNKTRIDEANQ 194

RESULT 4
Q8AXM2 PRELIMINARY; PRT; 206 AA.
ID Q8AXM2
AC Q8AXM2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP25a.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF335586; AAO13788.1; -.
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00835; SNAP-25; 1.
DR Pfam: PF05739; SNARE; 1.
DR SMART: SM00397; t_SNARE; 2.
DR PROSITE: PS50192; t_SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 89.9%; Score 80; DB 13; Length 206;
Best Local Similarity 88.9%; Pred. No. 7.3e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
DB 180 RIMEKADSNKTRIDEANQ 197

RESULT 5
Q8AXM1 PRELIMINARY; PRT; 206 AA.
ID Q8AXM1
AC Q8AXM1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DE [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

```

RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Ioshizuka S., Carninci F., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RP "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF335887; AA013789.1; -;
 DR EMBL; BC055981; AAH55981.1; -;
 DR InterPro; IPR000928; SNAP-25.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNAP-25; 2.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; t_SNARE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 206 AA; 23187 MW; 7D3B2071E577F02 CRC64;
 Query Match 89.9%; Score 80; DB 13; Length 206;
 Best Local Similarity 88.9%; Pred. No. 7.3e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 DB 180 RIMEKADSNKTRIDEANQ 197
 RESULT 6
 Q8JIS7 PRELIMINARY; PRT; 204 AA.
 AC Q8JIS7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP-23.
 GN XOSNAP-23.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mashima J., Nagahama M., Hattuzawa K., Tani K., Kikuchi F.,
 RA Horigome T., Yamamoto A., Tagaya M.;
 RT "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion
 RT of nuclear membrane vesicles.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033718; BAC06591.1; -;

DR InterPro; IPR000928; SNAP-25.
 DR Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Ioshizuka S., Carninci F., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RP "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF335887; AA013789.1; -;
 DR EMBL; BC055981; AAH55981.1; -;
 DR InterPro; IPR000928; SNAP-25.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNAP-25; 2.
 DR SMART; SM00397; t_SNARE; 2.
 DR PROSITE; PS0192; t_SNARE; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 206 AA; 23187 MW; 7D3B2071E577F02 CRC64;
 Query Match 89.9%; Score 80; DB 13; Length 206;
 Best Local Similarity 88.9%; Pred. No. 7.3e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RIMEKADSNKTRIDEANQ 18
 DB 180 RIMEKADSNKTRIDEANQ 197
 RESULT 6
 Q8JIS7 PRELIMINARY; PRT; 204 AA.
 AC Q8JIS7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SNAP-23.
 GN XOSNAP-23.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mashima J., Nagahama M., Hattuzawa K., Tani K., Kikuchi F.,
 RA Horigome T., Yamamoto A., Tagaya M.;
 RT "Evidence for the involvement of alpha-SNAP and SNAP-23 in the fusion
 RT of nuclear membrane vesicles.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB033718; BAC06591.1; -;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY092757; AAM18191.1; -.
 DR PDB; 1L4A; 31-JUL-02.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; T_SNARE; 2.
 DR PROSITE; PSS0192; T_SNARE; 2.
 SQ SEQUENCE 212 AA; 23816 MW; 127601619DE79E2D CRC64;

Query Match 72.0%; Score 65; DB 5; Length 212;
 Best Local Similarity 66.7%; Pred. No. 0.019; Indels 0; Gaps 0;
 Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEANQ 18
 :||:|||||:
 Db 187 RIQKAESESIDEANK 204

RESULT 9

035620 PRELIMINARY; PRT; 210 AA.
 AC 035620;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE 23kDa synaptosomal associated protein.
 GN SNAP23 OR MSNAP-23.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olken S.K., Doerre S., Corley R.B.;
 RT "SNARE expression in mouse plasma cells."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF007169; AAB62932.1; -.
 DR MGD; MGI:109356; Snap23.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; T_SNARE; 2.
 DR PROSITE; PSS0192; T_SNARE; 2.
 SQ SEQUENCE 210 AA; 23277 MW; FB/52FB58D5AE6D9 CRC64;

Query Match 66.3%; Score 59; DB 11; Length 210;
 Best Local Similarity 70.6%; Pred. No. 0.17; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
 :||:|||||:
 Db 185 KITEKADTKNRIDIAN 201

RESULT 10

070377 PRELIMINARY; PRT; 210 AA.
 AC 070377;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE SNAP-23.
 GN SNAP-23.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brownstein M.J., Bult C., Fletcher C., Carninci P., de Bonaldo M.F.,
 BLAKE J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA St-Denis J.F., Cabaniols J.P., Cushman S.W., Roche P.A.;
 RT "SNAP-23 participates in SNARE complex assembly in rat adipose cells."
 RL Biochem. J. 338:709-715 (1999).
 DR EMBL; AF052596; AAC06031.1; -.
 DR InterPro; IPR000928; SNAP-25.
 DR InterPro; IPR000727; T_SNARE.
 DR Pfam; PF00835; SNAP-25; 1.
 DR Pfam; PF05739; SNARE; 1.
 DR SMART; SM00397; T_SNARE; 2.
 DR PROSITE; PSS0192; T_SNARE; 2.
 SQ SEQUENCE 210 AA; 23235 MW; OD63E3A6F9FE3BA2 CRC64;

Query Match 66.3%; Score 59; DB 11; Length 210;
 Best Local Similarity 70.6%; Pred. No. 0.17; Indels 0; Gaps 0;
 Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RIMEKADSNKTRIDEAN 17
 :||:|||||:
 Db 185 KITEKADTKNRIDIAN 201

RESULT 11

009044 PRELIMINARY; PRT; 210 AA.
 AC 009044;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE SYDET (SNAP-23) (Synaptosomal-associated protein, 23KD).
 GN SNAP23 OR SNDT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Fat;
 RC MEDLINE=97312558; PubMed=9168999;
 RA Araki S., Tamori Y., Kawanishi M., Shinoda H., Masugi J., Mori H.,
 Niki T., Okazawa H., Kubota T., Kasuga M.;
 RT "Inhibition of the binding of SNAP-23 to syntaxin 4 by Munc18c."
 RL Biochem. Biophys. Res. Commun. 234:257-262 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9720227; PubMed=9067602;
 RA Wang G., Witkin J.W., Hao G., Bankaitis V.A., Scherer P.E.,
 Baldini G.;
 RT "Syndet is a novel SNAP-25 related protein expressed in many tissues."
 RL J. Cell Sci. 110:505-513 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ;
 RA Vaidyanathan V.V., Roche P.A.;
 RT "Structure and chromosomal localization of the mouse SNAP-23 gene."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schriml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Bono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RL	Nature 409-685-690(2001).
DR	EMBL; AK017311; SAG30866.1; --.
DR	MGI; MGI:109356; Snap23.
DR	InterPro; IPR000928; SNAP-25.
DR	InterPro; IPR000727; T_SNARE.
DR	Pfam; PF00835; SNAP-25; 1.
DR	Pfam; PF05739; SNARE; 1.
DR	SMART; SM00397; t_SNARE; 2.
DR	PROSITE; PS50192; T_SNARE; 2.
SQ	SEQUENCE 221 AA; 24550 MW; 368662BE7232DFFB CRC64;
 Query Match 66.3%; Score 59; DB 11; Length 221; Best Local Similarity 70.6%; Pred. No. 0.18; Matches 12; Conservative 2; Mismatches 3; Indels 0;	
QY	1 RIMEKADSNKTRIDEAN 17 : :
DB	196 KITERADTNKRIDIAN 212 : :
 RESULT 13	
O96578	PRELIMINARY; PRT; 90 AA.
ID	O96578;
AC	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Synaptosome-associated protein SNAP-25-5 (Fragment).
DE	SNAP-5.
GN	Leucophaea maderae (Madeira cockroach).
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC	Blaberidae; Leucophaea.
RN	NCBI_TaxID=6988;
RX	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=99259578; PubMed=10327594;
RR	Johard H.A., Risinger C., Naesel D.R., Larhammar D.;
RT	"The highly conserved synapse protein SNAP-25 displays sequence variability in the cockroach Leucophaea maderae.";
RT	Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 122:63-68(1999)
RL	EMBL; AF091602; AAC69878.1; --.
DR	InterPro; IPR000928; SNAP-25.
DR	InterPro; IPR000727; T_SNARE.
DR	Pfam; PF00835; SNAP-25; 1.
DR	Pfam; PF05739; SNARE; 1.
DR	SMART; SM00397; t_SNARE; 1.
DR	PROSITE; PS50192; T_SNARE; 1.
FT	NON TER 1
SQ	SEQUENCE 90 AA; 10136 MW; E50D28954676B9F7 CRC64;
 Query Match 56.2%; Score 50; DB 5; Length 90; Best Local Similarity 61.1%; Pred. No. 2.1; Matches 11; Conservative 2; Mismatches 5; Indels 0;	
QY	1 RIMEKADSNKTRIDEANO 18 : :
DB	66 RIKNKAESNEERIKVNO 83 : :
 RESULT 14	
O96576	PRELIMINARY; PRT; 125 AA.
ID	O96576
AC	O96576;
DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Synaptosome-associated protein SNAP-25-3 (Fragment).
GN	SNAP-3.
OS	Leucophaea maderae (Madeira cockroach).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC	Blaberidae; Leucophaea.

Search completed: March 9, 2004, 11:09:35

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 22.4211 Seconds
(without alignments)
84.434 Million cell updates/sec

Title: US-10-030-485A-2

Perfect score: 30

Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	18	Q9TRF1	Q9trf1 bos taurus
2	30	100.0	82	Q8MZ33	Q8mz33 drosophila
3	30	100.0	82	Q8IQC6	Q8iqc6 drosophila
4	30	100.0	107	Q8N3E7	Q8n3e7 homo sapien
5	30	100.0	149	Q82XY8	Q82xy8 rhizobium m
6	30	100.0	206	Q8AXM2	Q8axm2 xenopus lae
7	30	100.0	206	Q8AXM1	Q8axm1 xenopus lae
8	30	100.0	216	Q7Z390	Q7z390 homo sapien
9	30	100.0	297	Q8N417	Q8n417 homo sapien
10	30	100.0	507	Q86VG8	Q86vg8 homo sapien
11	30	100.0	537	Q9W2P0	Q9w2p0 drosophila
12	30	100.0	760	Q7XR85	Q7xr85 oryza sativ
13	30	100.0	904	Q8IWC1	Q8iwc1 homo sapien
14	27	90.0	21	Q87583	Q87583 chimpanzee
15	27	90.0	81	Q7V6N4	Q7v6n4 prochloroco
16	27	90.0	87	Q8BT51	Q8bt51 mus musculus

17	27	90.0	96	4	Q9NYJ1	Q9nyj1 homo sapien
18	27	90.0	105	4	Q96G37	Q96g37 homo sapien
19	27	90.0	112	16	Q541I3	Q541i3 streptomyce
20	27	90.0	117	16	Q9A4F3	Q9a4f3 caulobacter
21	27	90.0	122	4	Q9BTB7	Q9btb7 homo sapien
22	27	90.0	128	16	Q8PFC6	Q8pfc6 xanthomonas
23	27	90.0	130	15	Q76943	Q76943 human immun
24	27	90.0	135	16	Q8P3U7	Q8p3u7 xanthomonas
25	27	90.0	148	10	Q84MC4	Q84mc4 arabidopsis
26	27	90.0	162	16	Q66898	Q66898 aquifex ae
27	27	90.0	165	10	Q9XHP7	Q9xhp7 ceratopter
28	27	90.0	209	16	Q88Q68	Q88q68 pseudomonas
29	27	90.0	210	2	Q9RPM1	Q9rpx1 bacillus me
30	27	90.0	210	10	Q9SE48	Q9se48 oryza sativ
31	27	90.0	210	10	Q9SE47	Q9se47 oryza sativ
32	27	90.0	210	10	Q7X140	Q7x140 oryza sativ
33	27	90.0	222	5	Q8SXX3	Q8sxx3 drosophila
34	27	90.0	238	4	Q86TV0	Q86tv0 homo sapien
35	27	90.0	252	16	Q99YW2	Q99yw2 streptococc
36	27	90.0	252	16	Q8K6S1	Q8k6s1 streptococc
37	27	90.0	256	16	Q8E6N2	Q8e6n2 streptococc
38	27	90.0	256	16	Q8E178	Q8e178 streptococc
39	27	90.0	257	16	Q9HU49	Q9hu49 pseudomonas
40	27	90.0	257	16	Q8PMK9	Q8pmk9 xanthomonas
41	27	90.0	258	16	Q8PAV7	Q8pav7 xanthomonas
42	27	90.0	264	16	Q9RS89	Q9rs89 deinococcus
43	27	90.0	275	10	Q8H688	Q8h688 oryza sativ
44	27	90.0	283	10	Q43S08	Q43s08 lycopersico
45	27	90.0	284	16	Q98GM6	Q98gm6 rhizobium l

ALIGNMENTS

RESULT 1

ID Q9TRF1 PRELIMINARY; PRT; 18 AA.
AC Q9TRF1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Soluble N-ethylmaleimide-sensitive attachment protein SNAP-25
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93374072; PubMed=8365494;
RA Horikawa H.P., Saisu H., Ishizuka T., Sekine Y., Tsugita A., Odani S.,
RA Abe T.;
RL FEBS Lett. 330:236-240(1993).
SQ SEQUENCE 18 AA; 2120 MW; 371FC9376C4A7BB CRC64;

Query Match 100.0%; Score 30; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.3; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

Qy 1 EEMQRR 6
Db 2 EEMQRR 7

RESULT 2

ID Q8MZ33 PRELIMINARY; PRT; 82 AA.
AC Q8MZ33;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RE03722p.

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GN BCNDA:RE03722.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celnik S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY113381; AAM29386.1; -
DR FlyBase: FBgn063077; BCNDA:RE03722.
SQ SEQUENCE 82 AA; 9539 MW; E0F4D3104060796E CRC64;

Query Match 100.0%; Score 30; DB 5; Length 82;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
Db 58 EMOQR 63

RESULT 3
Q81QC6 PRELIMINARY; PRT; 82 AA.
ID Q81QC6;
AC Q81QC6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG32039-PA.
GN CG32039.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2019c006; PubMed=1071132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Fiamkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resse M.G.,

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RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
SC Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busan D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003552; AAN11959.1; -
DR FlyBase: FBgn052039; CG32039.
SQ SEQUENCE 82 AA; 9540 MW; E0FE73104AC0796E CRC64;

Query Match 100.0%; Score 30; DB 5; Length 82;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EMOQR 6
Db 58 EMOQR 63

RESULT 4
Q8N3E7 PRELIMINARY; PRT; 107 AA.
ID Q8N3E7;
AC Q8N3E7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
GN DXF27611323.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RR SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF335586; AAC13788.1; -;
DR InterPro: IPR000928; SNAP-25.
DR InterPro: IPR000727; T_SNARE.
DR Pfam: PF00833; SNAP-25; 1.
DR Pfam: PF05739; SNARE; 1.
DR SMART: SM00397; t SNARE; 2.
DR PROSITE: PS50192; T SNARE; 2.
SQ SEQUENCE 206 AA; 23122 MW; 2D1D0FD35E0C1DDF CRC64;

Query Match 100.0%; Score 30; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. NO. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 EEMQRR 6
|||
DB 12 EEMQRR 17

RESULT 7
QBAXMI PRELIMINARY; PRT; 206 AA.
ID QBAXMI
AC QBAXMI;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE SNAP25b (Hypothetical protein).frag).
OS xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RR SEQUENCE FROM N.A.
RA Kolk S.M., Groffen A.J.A., Tuinhof R., Verhage M., Roubos E.W.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
[2]
RR SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
[3]
RR SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strauberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF335587; AA013789.1; -.
DR EMBL; BC055981; AAH55981.1; -.
DR InterPro; IPR000928; SNAP-25.
DR InterPro; IPR000727; T SNARE.
DR Pfam; PF00835; SNAP-25; 1.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; T SNARE; 2.
DR PSORT; PS0192; T SNARE; 2.
KW Hypothetical protein.
SQ SEQUENCE 206 AA; 23187 MW; 7D3B20717E577F02 CRC64;

Query Match 100.0%; Score 30; DB 13; Length 206;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 12 EEMQRR 17

RESULT 8
Q72390 PRELIMINARY; PRT; 216 AA.
ID Q72390
AC Q72390
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZP686C04150 (Fragment).
GN DKFZP686C04150.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human colon endothel primary cell culture;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538046; CAD97985.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 216 AA; 24473 MW; 68CB647EB074786B CRC64;

Query Match 100.0%; Score 30; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 203 EEMQRR 208

RESULT 9
Q8N417 PRELIMINARY; PRT; 297 AA.
ID Q8N417
AC Q8N417
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Pancreas;
RA Strauberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC036844; AAH36844.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 297 AA; 32380 MW; 2AAB420A29422FEF CRC64;

Query Match 100.0%; Score 30; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 284 EEMQRR 289

RESULT 10
Q86VG8 PRELIMINARY; PRT; 507 AA.
ID Q86VG8
AC Q86VG8
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim N.-S., Shon H.-Y., Oh J.-H., Lee J.-Y., Kim J.-M., Hahn Y.,
RA Park H.-S., Kim S., Kim Y.S.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452716; AAP13351.1; -.
KW Hypothetical protein.
SQ SEQUENCE 507 AA; 54948 MW; EEA3E083E79CAD26 CRC64;

Query Match 100.0%; Score 30; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
Db 494 EEMQRR 499

RESULT 11
Q9W2P0 PRELIMINARY; PRT; 537 AA.
ID Q9W2P0
AC Q9W2P0
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE CG3221 protein (LD3682P).
GN CG3221.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaesner K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Iai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celnikier S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003452; AAF4650.1; -;
 DR EMBL; AY058678; AA113907.1; -;
 DR FlyBase; FBgn0034569; CG3221.
 SQ SEQUENCE 537 AA; 62576 MW; 94FBA570315F6FDF CRC64;

Query Match 100.0%; Score 30; DB 5; Length 537;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 DB 27 EEMQRR 32

RESULT 12
 QYXR85 PRELIMINARY; PRT; 760 AA.

AC QYXR85;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE OSNBA001107.16 protein.
 GN OSNBA001107.16.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
 RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
 RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
 RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,

RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
 RA Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
 RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
 RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
 RA Zhang R.Q., Guan J.P., Hong G.F.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL606587; CA802792.1; -;
 SQ SEQUENCE 760 AA; 82554 MW; 80C7507DACEB8643 CRC64;

Query Match 100.0%; Score 30; DB 10; Length 760;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 DB 320 EEMQRR 325

RESULT 13

QBIWCI PRELIMINARY; PRT; 904 AA.
 AC QBIWCI;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040518; AAH40518.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000515; BPD transp.
 DR Pfam; PF05672; E-MAP-115; 1.
 DR PROSITE; PS00402; BPD_TRANSP_INN_MEMBER; 1.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 904 AA; 101665 MW; 6C527C706D3EB11B CRC64;

Query Match 100.0%; Score 30; DB 4; Length 904;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 DB 652 EEMQRR 657

RESULT 14

QBIWCI PRELIMINARY; PRT; 21 AA.
 AC QBIWCI;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Rev protein (fragment).
 GN REV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=P051;
 RX MEDLINE=97138325; PubMed=8985351;
 RA Bibollet-Ruche F., Brengues C., Galat-Luong A., Galat G., Pourrut X.,

RA Vidal N., Veas F., Durand J.P., Cuny G.;
 RT "Genetic diversity of simian immunodeficiency viruses from west
 RT African green monkeys: evidence of multiple genotypes within
 RT populations from the same geographical locale.";
 RL J. Virol. 71:307-313(1997).
 DR EMBL; U37201; AAC56137.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR000625; REV_protein.
 DR Pfam; PF00424; REV; 1.
 DR NON TER 21
 SQ SEQUENCE 21 AA; 2599 MW; 6AD581D9CFE92914 CRC64;

Query Match 90.0%; Score 27; DB 15; Length 21;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 ||:||||
 Db 6 EELQRR 11

RESULT 15

QYV6N4 PRELIMINARY; PRT; 81 AA.
 ID QYV6N4
 AC QYV6N4;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Conserved hypothetical.
 GN PMT1118.
 OS Prochlorococcus marinus (strain MIT 9313).
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=74547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825698; PubMed=12917642;
 RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
 RT niche differentiation.";
 RL Nature 424:1042-1047(2003).
 DR EMBL; BX572098; CAE21293.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 81 AA; 9436 MW; BE9BD0715DAE40E8 CRC64;

Query Match 90.0%; Score 27; DB 16; Length 81;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
 ||:||||
 Db 62 EELQRR 67

Search completed: March 4, 2004, 08:29:14
 Job time : 24.4211 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 4, 2004, 08:25:19 ; Search time 8.21053 Seconds
(without alignments)
70.294 Million cell updates/sec

Title: US-10-030-485A-2
Perfect score: 30
Sequence: 1 EEMQRR 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	56	2 S36812	probable synapse-a
2	30	100.0	149	2 D95399	protein [imported
3	30	100.0	206	2 A37861	synaptosomal-assoc
4	30	100.0	206	2 153735	nerve terminal pro
5	30	100.0	206	2 167823	synaptosomal-assoc
6	30	100.0	206	2 A33623	SNAP-25 protein -
7	30	100.0	249	2 S38308	SNAP-25 protein -
8	30	100.0	249	2 S38309	hypothetical prote
9	27	90.0	112	2 T34589	hypothetical prote
10	27	90.0	117	2 C87594	hydrogenase matura
11	27	90.0	162	1 P70358	conserved hypothet
12	27	90.0	257	2 C93005	carbonic anhydrase
13	27	90.0	264	2 D75298	G-box-binding prot
14	27	90.0	283	2 S42393	pyrroloquinoline q
15	27	90.0	303	2 S58243	conserved hypothet
16	27	90.0	309	2 B69200	proline dehydrogen
17	27	90.0	319	2 C81892	hypothetical prote
18	27	90.0	337	2 T06602	hypothetical prote
19	27	90.0	333	2 T05121	LiM domain-contain
20	27	90.0	378	2 JC5658	HD GYP hydrolase d
21	27	90.0	407	2 C37212	adenylosuccinate l
22	27	90.0	450	2 C75033	probable adenylosu
23	27	90.0	450	2 H71135	hypothetical prote
24	27	90.0	453	2 S52690	conserved hypothet
25	27	90.0	472	2 A83239	probable glu-tRNA
26	27	90.0	509	2 A71254	conserved hypothet
27	27	90.0	528	2 B75310	serine-rich protei
28	27	90.0	534	2 T39903	SPC72 protein - ye
29	27	90.0	622	2 S51972	

30	27	90.0	647	2 C71534	probable transglyc
31	27	90.0	689	2 S17875	polynucleotide ade
32	27	90.0	702	2 C69999	DNA translocase st
33	27	90.0	727	2 S54512	hypothetical prote
34	27	90.0	739	2 S18642	polynucleotide ade
35	27	90.0	740	2 S17925	polynucleotide ade
36	27	90.0	783	2 AF1275	DNA translocase ho
37	27	90.0	784	2 AF1638	DNA translocase ho
38	27	90.0	809	1 Q08E34	BLF4 protein - hu
39	27	90.0	856	2 T13159	ELB-55kDa-associat
40	27	90.0	869	2 A25945	coagulation factor
41	27	90.0	947	2 B86231	hypothetical prote
42	27	90.0	961	2 A55380	faciogenital dyspl
43	27	90.0	1203	2 T21275	hypothetical prote
44	27	90.0	1274	2 A89959	hypothetical prote
45	27	90.0	1328	2 AE2351	protoporphyrin IX

ALIGNMENTS

RESULT 1

S36812
probable synapse-associated 28K protein - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 07-May-1999
C:Accession: S36812
R:Horikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.
FEBS Lett. 330, 236-240, 1993
A:Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn
A:Reference number: S36811; MUID:93374072; PMID:8365494
A:Accession: S36812
A:Molecule type: protein
A:Residues: 1-56 <HOR>
A:Experimental source: brain

Query Match 100.0%; Score 30; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
| | | | |
DB 2 EEMQRR 7

RESULT 2

D95399
protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSyma
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: D95399
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: D95399
A>Status: preliminary
A:Box-binding prot
A:Molecule type: DNA
A:Residues: 1-149 <KUR>
A:Cross-references: GB:AE006469; PTIN:AAK65758.1; PID:gl4524256; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSyma
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:111474104
A:Contents: annotation
C:Genetics:
A:Gene: SMA2009


```

A:Genome: plasmid
Query Match      100.0%; Score 30; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 137 EEMQRR 142

RESULT 3
A37861
synaptosomal-associated 25K protein - chicken
C:Species: Gallus gallus (Chicken)
C>Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 21-Jul-2000
C:Accession: A37861
R:CatSicas, S.; Larhammar, D.; Blomqvist, A.; Sanna, P.P.; Milner, R.J.; Wilson, M.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 785-789, 1991
A:Title: Expression of a conserved cell-type-specific protein in nerve terminals coincides with the expression of a conserved cell-type-specific protein in nerve terminals
A:Reference number: A37861; MUID:91126080; PMID:1992470
A:Accession: A37861
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <CAT>
A:Cross-references: GB:M57957; NID:g212673; PIDN:AAA49072.1; PID:g212674

Query Match      100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 12 EEMQRR 17

RESULT 4
I53735
nerve terminal protein - human
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I53735
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I53735; MUID:94156217; PMID:8112622
A:Accession: I53735
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:U19760; NID:g307425; PIDN:AAC37545.1; PID:g307426
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match      100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 12 EEMQRR 17

RESULT 5
I67823
nerve terminal protein - human
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C:Accession: I67823
R:Bark, I.C.; Wilson, M.C.
Gene 139, 291-292, 1994
A:Title: Human cDNA clones encoding two different isoforms of the nerve terminal protein
A:Reference number: I67823; MUID:94156217; PMID:8112622
A:Accession: I67823
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-206 <RES>
A:Cross-references: GB:U19761; NID:g307427; PIDN:AAC37546.1; PID:g307428
C:Genetics:
A:Gene: GDB:SNAP
A:Cross-references: GDB:355671; OMIM:600322
A:Map position: 20p11.2-20p11.2

Query Match      100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 12 EEMQRR 17

RESULT 6
A33623
synaptosomal-associated 25K protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Apr-1990 #sequence_revision 04-Apr-1990 #text_change 05-Nov-1999
C:Accession: A33623
R:Oyler, G.A.; Higgins, G.A.; Hart, R.A.; Battenberg, E.; Billingsley, M.; Bloom, F.E.;
J. Cell Biol. 109, 3039-3052, 1989
A:Title: The identification of a novel synaptosomal-associated protein, SNAP-25, differs from the previously identified SNAP-25
A:Reference number: A33623; MUID:90078337; PMID:2592413
A:Accession: A33623
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <OYL>
A:Cross-references: GB:M22012; GB:X51673; NID:g200997; PIDN:AAA61741.1; PID:g200998

Query Match      100.0%; Score 30; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 12 EEMQRR 17

RESULT 7
S38308
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38308
R:Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis-
tinct isoforms of the protein
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38308
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 194/3

Query Match      100.0%; Score 30; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
    |||||
Db 12 EEMQRR 17

```

RESULT 8

S38309
SNAP-25 protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 09-Jun-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S38309
J. Bark, I.C.
J. Mol. Biol. 233, 67-76, 1993
A:Title: Structure of the chicken gene for SNAP-25 reveals duplicated exons encoding dis
A:Reference number: S38308; MUID:93389738; PMID:8377193
A:Accession: S38309
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-249 <BAR>
A:Cross-references: EMBL:L09250
C:Genetics:
A:Introns: 24/3; 38/3; 55/1; 94/2; 136/2; 184/3

Query Match 100.0%; Score 30; DB 2; Length 249;

Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
DB 12 EEMQRR 17

RESULT 9

T34589
hypothetical protein SC10A5.22 SC10A5.22 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
A:Accession: T34589
R. Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z21548
A:Accession: T34589
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-112 <NUR>
A:Cross-references: EMBL:AL021529; PIDN:CAA16454.1; GSPDB:GN00070; SCOEDB:SC10A5.22
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC10A5.22

Query Match 90.0%; Score 27; DB 2; Length 112;

Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
DB 97 EELQRR 102

RESULT 10

C87594
hypothetical protein CC2787 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: C87594
R. Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Emolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: C87594
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <STO>
A:Cross-references: GB:AE005673; NID:gl3424387; PIDN:AAK24751.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2787

Query Match 90.0%; Score 27; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEMQRR 6
|||
DB 74 DEMQRR 79

RESULT 11

F70358
hydrogenase maturation factor hupD [similarity] - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Mar-2003
C:Accession: F70358
R. Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70358

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-162 <AQF>

A:Cross-references: GB:AE000701; GB:AE000657; NID:g2983260; PIDN:AAC06858.1; PID:g29832
A:Experimental source: strain VF5
C:Genetics:
A:Gene: hupD
C:Superfamily: [Nife]-hydrogenase maturation protease

Query Match 90.0%; Score 27; DB 1; Length 162;
Best Local Similarity 83.3%; Pred. No. 95;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
DB 23 EELQRR 28

RESULT 12

C83005
conserved hypothetical protein PA5135 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83005
R. Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Harbig, K.; Lim
; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: C83005

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AAG08520.1; GSPDB:GN00

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA5135

Query Match 90.0%; Score 27; DB 2; Length 257;

Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
|||
DB 143 EELQRR 148

RESULT 13

D75298
carbonic anhydrase - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75298
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75298
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-264 <WHI>
A:Cross-references: GB:AE002056; GB:AE000513; NID:96460037; PIDN:AAF11784.1; PID:9646004
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR2238
A:Map position: 1
C:Superfamily: Escherichia coli carbonate dehydratase

Query Match 90.0%; Score 27; DB 2; Length 264;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 34 EELQRR 39

RESULT 14

S42393
G-box-binding protein - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Sep-2000
C:Accession: S42393
R:Meier, I.; Gruissem, W.
Nucleic Acids Res. 22, 470-478, 1994
A:Title: Novel conserved sequence motifs in plant G-box binding proteins and implication
A:Reference number: S42392; MUID:94173701; PMID:8127687
A:Accession: S42393
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-283 <MEI>
A:Cross-references: EMBL:X74942; NID:9456752; PIDN:CAA52896.1; PID:9456753
C:Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
F:182-222/Domain: fos/jun DNA-binding domain homology <FJD>

Query Match 90.0%; Score 27; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 213 EELQRR 218

RESULT 15

S58243
pyrroloquinoline quinone synthesis B - Pseudomonas fluorescens
C:Species: Pseudomonas fluorescens
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-Oct-1999
C:Accession: S58243
R:Schneider, U.; Keel, C.; Defago, G.; Haas, D.
submitted to the EMBL Data Library, May 1995
A:Description: Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHAO: thei
A:Reference number: S58239
A:Accession: S58243
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <SCH>
A:Cross-references: EMBL:X87299; NID:9929799; PIDN:CAA60733.1; PID:9929805

Query Match 90.0%; Score 27; DB 2; Length 303;

Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEMQRR 6
DB 227 DEMQRR 232

Search completed: March 4, 2004, 08:29:53
Job time : 10.2105 secs